

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2004, 16:15:20 ; Search time 4236 Seconds

(without alignments)
10426.099 Million cell updates/sec

Title: US-10-807-228-2

Perfect score: 1212
Sequence: 1 ATGACTGACGACATGTGCA.....AACACACATCATCGCAAC 1212

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing filter 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322.6	26.6	470	4	B1376242 BFLG3_000
2	221	18.2	470	1	A1906433 IL-BT109-
3	207.8	17.1	494	6	CD307119 StrPu691.
4	188.6	15.6	442	6	CD295681 StrPu691.
5	123.6	10.2	519	6	CD296311 StrPu691.
6	83.2	6.9	551	7	CF919042 BEL0531.
7	83.2	6.9	553	4	B1387857 BFLG3_002
8	63.6	5.7	524	8	BZ894814 H94_0102
9	63.2	5.7	722	6	CB656525 OSJNEC10P
10	67.6	5.6	722	6	CB683938 OSJNEC10P
11	63.6	5.2	925	9	CN80091P AL053013 Drosophila
12	60.8	5.0	712	6	CD869465 AZ02.111L
13	60.8	5.0	812	6	CB659172 OSJNEC10
14	60.6	5.0	604	1	AU162766
15	60.6	5.0	668	1	CD225047 CCCI_37_H
16	60.4	5.0	512	4	BM140351 WHE0474_a
17	60.2	5.0	719	4	CF487085 POL1_41.D
18	60	5.0	748	7	CN143339 WOUND1_15
19	60	5.0	768	7	CN148454 WOUND1_56
20	60	5.0	814	7	CN126847 RH0H1_19
21	60	5.0	1115	7	CK208301 FGAS02000
22	59.8	4.9	635	6	CA254345 SCBFL411
23	59.8	4.9	707	7	CF874011 tric035xc
24	59.8	4.9	732	7	CF866540 tric030xc

25	59.8	4.9	748	6	CA227320	CA227320
26	59.8	4.9	762	6	CB903555	CB903555 tric03555
27	59.8	4.9	803	6	CB902534	CB902534 tric030xc
28	59.6	4.9	683	6	CA269770	CA269770 SCWCR308
29	59.4	4.9	670	6	CD429468	CD429468 ETH1_4 DO
30	59	4.9	579	2	BE040798	BE040798 OF1G11 O
31	59	4.9	690	2	BE041110	BE041110 OF19H01 O
32	59	4.9	806	7	CN127041	CN127041 RH0H1_20
33	58.8	4.9	888	9	CG440030	CG440030 OCWHP10TH
34	58.6	4.8	532	4	BG241153	BG241153 OV1_38_HO
35	58.6	4.8	635	6	CD223689	CD223689 CCCI_29_A
36	58.6	4.8	641	7	CF481017	CF481017 POL1_69_B
37	58.6	4.8	646	6	CD229216	CD229216 CCCI_13_A
38	58.6	4.8	660	6	CD227467	CD227467 CCCI_51-FG
39	58.6	4.8	664	7	CN133040	CN133040 OX1_5_F05
40	58.6	4.8	666	6	CD222873	CD222873 CCCI_24_F
41	58.6	4.8	667	7	CF485910	CF485910 POL1_34_B
42	58.6	4.8	672	6	CD224549	CD224549 CCCI_34_E
43	58.6	4.8	680	7	CF432900	CF432900 NIT1_19_E
44	58.6	4.8	703	7	CF487230	CF487230 POL1_42-C
45	58.6	4.8	710	7	CF488266	CF488266 POL1_48-F

ALIGNMENTS

RESULT 1
B1376242
LOCUS
DEFINITION
BFLG3_000038 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGP498) Branchiostoma floridae cDNA clone MPMGP498A1518 5', mRNA sequence.

ACCESSION
B1376242
VERSION
B1376242.1 GI:30911206
KEYWORDS
EST.
SOURCE
Branchiostoma floridae (Florida lancelet)
ORGANISM
Branchiostoma floridae

REFERENCE
AUTHORS
Panopoulou, G., Hennig, S., Groch, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
TITLE
New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes

JOURNAL
MEDLINE
PUBMED
COMMENT
Genome Res. 13 (6A), 1056-1066 (2003)
12799346
Contact: Panopoulou G
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Fax: +49 30 8413 1128
Email: panopoulou@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One cluster per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.rzpd.de>)
PCR primers
FORWARD: 5' CCCAGGCTTACCTTATGCTTCGCGCTCG 3' (M13SP)
BACKWARD: 5' GCTATTACGACGACGCGAAGGGGATGCG 3' (M13SP)
Insert length: 1200 Std Error: 0.00
Seq primer: 5'-CCGCGCGAATGTCGGCGGT-3' pSPORT3/86
High quality sequence stop: 623.

FEATURES

Location/Qualifiers

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/organism="Branchiostoma floridae"
/mol_type="mRNA"
/db_xref="taxon:7739"
/clone="MPMGp498A1518"
/clone_type="whole embryo"
/dev_stage="5-6 hrs (gastrula stage)"
/clone_lib="E.coli, XLI blue"
convention: BFLG or MPMGp498"
/note="Vector: pSport1; Site 1: SalI, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); Oligodt primed and directionally cloned in pSport1 vector using a NotI (5'-TGACCTGAGTCTGATGCGGAGCGCGCCG (T)15-3' and a SalI 5'-TCGACCCGCGCTCG-3' adapters (Gibco BRL)."

ORIGIN

Query Match 26.6%; Score 322.6; DB 4; Length 623;
Best Local Similarity 70.4%; Pred. No. 1.4e-60;
Matches 430; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 570 GCCGAGCATGAGTGGCGATCCGACCAATGCGATGATCCGAGATCCGCAATC 629
DB 13 GCGTAGTACGAGCTGGCGATGACGCGCTCCAAACAATGATACGGGAATGCCAGAC 72
QY 630 GTTCCCTTCTGAGAGCTGATGACACCTGAGACTGCTGCTCCGCGCATCAACCGA 689
DB 73 CTACCCGATGGGGAATCATGACACTTGGGCGCTGATCCAGTCCAGGATCAACACTGA 132
QY 690 CGGCGGCAATCCGCGTACCAACGCGATCCGCGATCCGCGATCCCTTCCGCTCA 749
DB 133 CGGAGGACACACCTCTGACGTCACGCGCGCGGCGAGTGGGAGATCCTTGTCATCA 192
QY 750 CACCTTCCGAGTATCTTGGGCTACTACACCGCGCTGAGAGCGCACGCTGCTGCGACCA 809
DB 199 CACCTTCCGAGTATGCGGGGATACATTTGCGATGAGAGAGAGACGATCCTGTAACA 252
QY 810 TGTCCATGACCGCAGCTGACATCTGGGAGAGAACTGGCGCGTCAATCCCGCGGCT 869
DB 253 CGCTTCCGAGCAGCACCTCCGACTTGGGAGATCACTGAAGTAACTACCGCGCGGCGCT 312
QY 870 CGAGCTGATCAAGCGCGCGCGCGCTGCAAGAGCATGCGCATCGAGCTCAACGAGATGA 929
DB 313 GAGAGCTATCCGCGCGGAGCGCGCTGCTGTCATGCACTGCACTGAGCTGAACGAGATGA 372
QY 930 CGCGAGTGGGAGACTGCTGTAAGTACCGCTCTTGGGCTATGGCACTCTTCCGCGTCT 989
DB 373 CGGAGGACACCGGCGCTGCTGACAGTACCGCGCATCGGCTACCTCTTGGGCTCAT 432
QY 990 GTGCACTACTAGCGTGCAGAGCGCGCGTGAAGCTGCGCGAGAGACATGACACCGAGCT 1049
DB 433 GTGCACTACTAGCGGAGGAGAGAGATTTGGAGCTGAGAGAGAGTCCATATACGCTCT 492
QY 1050 GAAAGCGCGCATGAGTGTCTCATGAGAGCGAGTGTGATGCTCCGAGAGGAGATGCCG 1109
DB 493 GAGAGCGCGGATGCTGTCTCATGAGAGCGAGTGTGATGCTCCGAGAGGAGATGCCG 552
QY 1110 TGCCGCGCGCTATCGGAGACGACATCTGATCTGCGGAGAGAGCGTCCGAGAGACT 1169
DB 553 ACCGCGCGGCTTACCGGAGACGACATCTTGTGTGATGAGAGAGCGGCGGAGAGACT 612
QY 1170 CACCGGCTTCC 1180
DB 613 TACAGGCTCC 623

RESULT 2
AI906433/c AI906433 470 bp mRNA linear EST 30-MAR-2000
LOCUS IL-BT109-280199-002 BT109 Homo sapiens cDNA, mRNA sequence.
DEFINITION AI906433
ACCESSION AI906433
VERSION AI906433.1 GI:6496820

KEYWORDS

EST.
Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS

1 (bases 1 to 470)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?l=il-BT109-002.html
kt3=280199&cl=1)
Seq primer: puc 18 forward.

FEATURES

Location/Qualifiers

1..470
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT109"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 18.2%; Score 221; DB 1; Length 470;
Best Local Similarity 69.4%; Pred. No. 3.2e-38;
Matches 313; Conservative 0; Mismatches 137; Indels 1; Gaps 1;

QY 630 GTTCCCTTCTGAGAGCTGATGACACCTGACCTGTTTCAAGTGGGAGATCAACCGA 689
DB 455 GATCCCTGAGTATGGGCGTATTAACCTTGAGCATGTTTCAAGTGGGAGATCAACCGA 396
QY 690 CGGCGGACAAATCCGGTACCAACCGCATGTGATCCGCGGAGATCTTTCCTCA 749
DB 395 TGGGCGGATTAACCGGATGACAGCGCGCGGAGAGAGAGAGATCTTTCCTCA 336
QY 750 CACCTTCCGAGTATCTTTCGCGC-TACTACACCGCGCTGAGAGAGAGCTTTCGAGC 808
DB 335 TTGCTTCCGATGATCCGCGGATTAACCGCGCTTGAAGGACAGCTTTCCTCA 276
QY 809 ATGTGATGACGACGCTTCGACATCTTGGAGAGAGAGAGTGGCGCGTGCATCCGCGGAGC 868
DB 275 ACTGCCGAGAGAGTACGCTGATGAGAGAGAGAGAGTGCAGATGACAGAGAGCGGAGC 216
QY 869 TCGAGCTATCAAGCGCGCGCGCGCTGCAAGAGATGCGATGAGTCAACAGAGAT 928
DB 215 TGAACATGTGCGCGCGCGCATGCGCTGACAGATGCTGCGGAGATGACAGAGAT 156
QY 929 ACCGAGATGAGAGCTGCTGAAGTACGCTCTTTCGCTATGAGCACTCTTTCGCGGAGC 988

DB 155 TCCTGGCCAGCAGCTGTGTGACGTACCGACCTTCGGTATGAGCACTGCTTCGGACCT 96

QY 988 TGTGCACCTACTAAGGTCCCGAGCGCGGTGAGTGTGGCCAGACATCGACACCGAGC 1048

DB 95 TGAGCCACACTAATGAGCCCGCNAAGCGGGCTGAGTGTGGCGAGCATCGACACGCTGC 36

QY 1049 TGAAGCCCGGCAATGGTGTCTCCATGAGCC 1079

DB 35 TGGAAACCGGACATGGTGTGTCTATCAGCGCC 5

RESULT 3
CD307119/c 494 bp mRNA linear EST 16-SEP-2003

LOCUS Strongylocentrotus purpuratus cDNA clone

DEFINITION MPMGP691E0990/MP1_SURUDI_90E9 5', mRNA sequence.

ACCESSION CD307119

VERSION CD307119.1 GI:34752168

KEYWORDS EST

SOURCE Strongylocentrotus purpuratus

ORGANISM Strongylocentrotus purpuratus

REFERENCE Pouskka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A., Reinhardt, R., Herwig, R., Panopoulou, G., and Lehrach, H. Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)

JOURNAL Contact: Pouskka AJ

COMMENT Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
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Fax: +49 30 8413 1128

Email: pouskka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONF) to reduce sequencing redundancy. According to the ONF procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (<http://www.tzpd.de>)

PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATGCTTCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACGCCAGTGGGAGAGGGAGATG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCCGAAATTCGGGT-3' pSPORT3/86

High quality sequence stop: 494.

Location/Qualifiers

1. 494

FEATURES

source

/organism="Strongylocentrotus purpuratus"

/mol_type="mRNA"

/db_xref="Caxon:7668"

/clone="MPMGP691E0990/MP1_SURUDI_90E9"

/cissue_type="whole larva"

/cissue="larva 2-3 weeks"

/dev_stage="B.coli, XLI Blue"

/clone_lib="Sea urchin larva cDNA library MPMGP691"

/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; Random primed and directionally cloned in pSPORT15 using a NotI (5'-pGACTGCTTCTAGATCGGACGCGCGCC (T)15-3' and a SalI 5'-TCGACCCACGCGCTCG-3' adapters (Gibco BRL)"

ORIGIN

Query Match 17.1%; Score 207.8; DB 6; Length 494;

Best Local Similarity 66.8%; Pred. No. 2.6e-35;

Matches 312; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

QY 730 GCGCAGATCCTTTCCTCAACACCTTCCGATGATCTTGGTACTACACCGCGCTGGAG 789

DB 476 GGTGACGGCATCTGCTTAACTCTTCCCTTATGATAGCGCGCTATTTCTCGCGCTTGA 417

QY 730 GCGCAGTCTTTCGCGCATGTCATGACCGCAGC---CTGCATCTGGGAGGAAG 846

DB 416 CGAACCTTTTCTTAAACACGTCGCTTCCAGCCGCATCTTGAAGTGTGGACGCTCAAC 357

QY 847 GTGGCCGTGATCGCCGCGGCTCGAGCTGATCAAGCCGCGCGCTGCAAGACATC 906

DB 356 TGGCAGCTTACACCGCGCGGATGAGGTCAATCAAGCCGTGTCAAAATGCTGCCAGTC 297

QY 907 GGCATCGAGCTCAACGATGTACCGCAGGTGGACCTGCTGAAGTACCGCTCTTCCGC 966

DB 236 GCGCTCGAGTTGAACGATGATACCGGAGGAACCTTACATCAAGATGAGCTTCGCGC 237

QY 967 TATGGCACTCTCTTGGGCTGTGCTGACACTACAGGTCGGGAGCGCGCTGAGCTG 1026

DB 236 TACGGGCACTCTTGGGCTGTGCTGACACTACAGGTCGGGAGCGCGCTTGAAGTTG 177

QY 1027 CGCAGACATCAACACCGAGCTGAAGCCGCGCATGTGTCTTCATGAGCCGATGTG 1086

DB 176 AGGGAAGACATCGACACTGTATATACAGCTGTGTATGTGCTTTCATGAGCCACATCTC 117

QY 1087 ATGCTCGCGAGGCGATCCCGGTGCGCGCTATCGCAGACACATCTGTATCGTC 1146

DB 116 ACGATACCAAGCGGACACTGTGTGCAAGAGGCTACAGGAGCATGATATCATGTTGTG 57

QY 1147 GGGAGGAGCGGTCCGAGACATCACCGGCTTCGCGTCCGCGCGGA 1193

DB 56 ACTGAAGAGGGCGCTTTCGATACCGGATTTCTTACGACCGGA 10

RESULT 4
CD295681 442 bp mRNA linear EST 16-SEP-2003

LOCUS Strongylocentrotus purpuratus cDNA clone

DEFINITION MPMGP691E0990/MP1_SURUDI_90E9 3', mRNA sequence.

ACCESSION CD295681

VERSION CD295681.1 GI:34746758

KEYWORDS EST

SOURCE Strongylocentrotus purpuratus

ORGANISM Strongylocentrotus purpuratus

REFERENCE Pouskka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A., Reinhardt, R., Herwig, R., Panopoulou, G., and Lehrach, H. Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)

JOURNAL Contact: Pouskka AJ

COMMENT Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inmestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128

Email: pouskka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONF) to reduce sequencing redundancy. According to the ONF procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA clones and filters are distributed via the Resource Center/Primary

Database of the German Human Genome Project (<http://www.rzpd.de>)

PCR Primers
FORWARD: 5' CCCAGCTTACACTTATGCTCCGGCTG 3' (M13SP) 5'-seq
BACKWARD: 5' GCTATTACGCGAGCGGAGGAGTG 3' (M13FSP) 3'-seq
Seq primer: 5' GCTATTACGCGAGCGGAGGAGTG 3' (M13FSP)
High quality sequence stop: 442.
Location/Qualifiers

FEATURES

source

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/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="MPMP691E0990:MPI SURUDI_90B9"
/cisue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMP691"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI; Random
primed and directionally cloned in pSport1 vector using a
NotI (5'-GACATGTTCAAGTGCAGCGCGCC (T)15-3' and a
SalI 5'-TCGACCCAGCGTCCG-3' adapters (Gibco BRL)"
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ORIGIN

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Query Match      15.6%; Score 188.6; DB 6; Length 442;
Best Local Similarity 67.3%; Pred. No. 4.4e-11;
Matches 282; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

QY 730 GCGGACATCTTTCGCTCAACACCTTCCGATATCTTGGCTACTACACCGCGCTGAG 789
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 GGTGACGGATCGTCTTAAACGCTTCCCTATATAGCCGGCTATTCTCGCGCTTGA 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 790 CGCAGCTGTTTCGACCATGTCATGAGCGGAGC---CTGACATCTGGGAGAAAG 846
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 CGAACCTTTTCTTGAACACAGTGCCTTCCGACCGGACATCTTGAAGTGGAGCTCAAC 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 847 GTGGCCGTGATCGCGCGGCTGAGCTATCAAGCCGCGCGCTGCAAGACATC 906
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 TCGACGTTACACGCGCGGAGATGAGCTCATCAAGCTGTCAATATGTCGACGTC 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 907 GGCATGAGCTCAACAGATGTAACCGGAGTGGAGACTGTGAAGTACCGCTCTTGGC 966
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 GCGCTGAGTTGAACAGATGTAACCGGAGAAAGAACTTCAAGTCAAGAGCTTGGC 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 967 TATGGCACTCTTCCGCGGTGCTGCACTACTACGTCGCGAGCGCGCGTGAAGCTG 1026
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 260 TAGGGCACTCTTCCGGGTCTTATGCACTACTACGCGCGGAGCAAGCTTGAAGTTG 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1027 CGCAGAGACATGACACCGAGTGAAGCCCGGATGATGATCTCATGAGCCGATGTG 1086
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 320 AGGAGAGACATGAGACTGTATACAGCTGTGATGCTTTCATGAGCCACATCTC 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1087 ATGCTGCCGAGGAGGATGCCCGGTGCGCGGCTATCGGAGACAGACATCTGATCT 1145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 380 ACGATAACAGAGGAGCAAGCGCTGTGAGAGGCTACAGAGAGCATATCATGGGTGT 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5

CD296311

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)

Contact: Poustka A.J.
Laboratory 145, Dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inmstr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128

Email: poustka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONP) to reduce sequencing redundancy. According to the ONP procedure, clones that display the same hybridisation matrix with a battery of 200 inner oligonucleotides are grouped into clusters. One clone per ONP cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONP cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (<http://www.rzpd.de>)

PCR Primers

FORWARD: 5' CCCAGCTTACACTTATGCTCCGGCTG 3' (M13SP) 5'-seq
BACKWARD: 5' GCTATTACGCGAGCGGAGGAGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CGGTCGGAATCCCGGT-3' pSport3/86
High quality sequence stop: 519.
Location/Qualifiers

FEATURES

source

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1..519
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/mol_type="mRNA"
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/dev_stage="larva 2-3 weeks"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMP691"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI; Random
primed and directionally cloned in pSport1 vector using a
NotI (5'-GACATGTTCAAGTGCAGCGCGCC (T)15-3' and a
SalI 5'-TCGACCCAGCGTCCG-3' adapters (Gibco BRL)"
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ORIGIN

```
Query Match      10.2%; Score 123.6; DB 6; Length 519;
Best Local Similarity 55.9%; Pred. No. 8.9e-17;
Matches 275; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

QY 10 GACATGTTGACGTTGATGAATGCAACGCGGAGAAAGTATTCCCGCTTTTCGAT 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 24 GAGATGCCAAGTTGATGACCTACGAAATGATGTAAGCGGCCACCAAGCTTCCACCC 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 GCGGAGTACCCCGCGGCAAAAGCAAGTTGCGGCTGATGAGCCAAAGCAATGCTAT 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 84 GCGGAGATGCAACGCGGTGAGAGCGCTCCGAGCCACATGCTGACCAAGGAATCGAA 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 130 GCGGCGTGTCACTCTTATCACTGATCACTACTTTCGCGGTGCTGACTAT 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 GCGTACTCTGACGTCATGACATCACTCAATCTTCTCGACTACTCTTACTGAC 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 TTGAGACCAAGTACGCGATGATCAAGCAACAGCAGCAGCATTTTCGCGCGC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 GTCGGTGTCTTCCGAGGCTTGTATCACTCAAGCAAGAGTGTCAACATGCTGCCCTC 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 250 ATCGAGGCGGCGAGCCTTGGCG-----CGCAGCTTGGGAGCAACATCACTCAAC 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 264 GTGCAACAGCGGCGAGGCTTGGCGAGATCAACCGTGAAGCAGATGTGTATTCACAG 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 GACTGGGCGGCGCAATTTCTATCGGCGGT---GGCGACGTCAGCAGCGGCGCAG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 324 GATTGGATCGCGAATCTTTCGAGCGCGCTTGGCACTGCTCTGGCAAGCCTTCGAG 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 CGCATCGGATCGAGTTGACACGATCATCTTCCGCGCGCAGCTCGAGAGACC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 384 AAGATCGAGCGAATTGATCATATACCTCATGAGAGAAACTTAAGTGAACAACT 443
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QY 421 CTACCGGGCGTGCATTCGACATCGACGAGCCCTCGATGTCGATCGGACACCATCAAG 480
 Db 444 GTATCTTCGAGACGACACCTCGATGTCGATTCACCATCGACGATCGAATCATCAAG 503
 QY 481 TCGCTCGAAGAG 492
 Db 504 TCCCGGAGAG 515
 RESULT 6
 CFP19042 551 bp mRNA linear EST 05-NOV-2003
 LOCUS BFL26-531.000127 Amphioxus 26 hrs cDNA library (Name convention: BFL26 or MPWG531) Branchiostoma floridae cDNA clone
 DEFINITION MPWG531L07115;BFL26_115L7 5', mRNA sequence.
 CFP19042
 CFP19042.1 GI:38190244
 EST.
 Branchiostoma floridae (Florida lancelet)
 SOURCE Branchiostoma floridae
 ORGANISM Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
 REFERENCE 1 (bases 1 to 551)
 Panopoulou, G., Hennig, S., Groth, D., Krause, A., Pousetka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
 New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes
 TITLE Genome Res. 13 (6A), 1056-1066 (2003)
 JOURNAL MEDLINE 22683279
 PUBMED 12799346
 COMMENT Contact: Panopoulou G
 Laboratory 145, dept. Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Ihnestr.63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1235
 Fax: +49 30 8413 1128
 Email: panopoul@molgen.mpg.de
 The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of all clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the clone project site at <http://www.molgen.mpg.de/amphioxus>.
 Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.tzpd.de>).
 PCR Primers
 FORWARD: 5' CCCAGGCTTACACTTATGCTCCGGCTG 3' (M13RSP)
 BACKWARD: 5' GCTATTACGCGACGTGGCAAGGGGATGTG 3' (M13FSP)
 Insert Length: 1200 Std Error: 200 00
 Seq primer: 5'-CCGCTCGGCAATCCCGGT-3' pSPORT3/86
 High quality sequence stop: 551.
 Location/Qualifiers
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 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /strain="wild type"
 /db_xref="taxon:7739"
 /clone="MPWG531L07115;BFL26_115L7"
 /issue_type="whole embryo"
 /dev_stage="26 hrs (neurula stage)"
 /lab_host="Escherichia coli, XL1 blue"
 /clone_lib="Amphioxus 26 hrs cDNA library (Name convention: BFL26 or MPWG531)"
 /note="Vector: pSPORT1; Site 1: SalI, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSPORT1 vector using a NotI (5'-GGACTAGTTCTAGATCGGAGCGCGGCC (T)15-3' and a SalI 5'-

ORIGIN TCGACCAAGCGTCCG-3'adapters (Gibco BRL)."
 Query Match 6.9%; Score 83.2; DB 7; Length 551;
 Best Local Similarity 57.8%; Pred. No. 6.9e-08;
 Matches 148; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 26 TGAATGGCAACAGCGGAGAAAGATTATTCGCCGTTTTCGGATGCCGAGATACCCGCC 85
 Db 286 TGGACATGATACAGCGGAGGAGTCACCAACCACTTCATGAGAGAACTCCAGAGAA 345
 QY 86 GCCAAAACAGCTTCGCGGCTGATGAGCCCAAGACATGTCATGCGGCGCTTCACT 145
 Db 346 GGCTGACAAAGCTGCGTCTCTCATGCTACGACAGTATATGATGACGCTCTTCACTT 405
 QY 146 CTATATCATCATCACTACTATTCGCGCTGCTACTGCTATTTGGACGCAATAGC 205
 Db 406 CCTATCATTAATCACTACTACTGCACTTCTGTACACTTCATTCGGTCCGACCTACG 465
 QY 206 GCATGTCATTCAGCACAACAGCCACAGCATTTGGCCGCAATCGAGCGGCACG 265
 Db 466 GGCTGCTCTTCACATGACCAAGTCTTCTTATCCCAAGCTTGAAGGTGTCACG 525
 QY 266 CCTGGCGCGCAGCTT 281
 Db 526 CCTGAGAGAGAGCAT 541
 RESULT 7
 B1387857 553 bp mRNA linear EST 26-AUG-2003
 LOCUS BFL26 002560 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPWG531) Branchiostoma floridae cDNA clone MPWG531L07115 5', mRNA
 DEFINITION sequence.
 ACCESSION B1387857
 VERSION B1387857.1 GI:30922696
 KEYWORDS EST.
 SOURCE Branchiostoma floridae (Florida lancelet)
 ORGANISM Branchiostoma floridae
 Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
 REFERENCE 1 (bases 1 to 553)
 Panopoulou, G., Hennig, S., Groth, D., Krause, A., Pousetka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
 New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes
 TITLE Genome Res. 13 (6A), 1056-1066 (2003)
 JOURNAL MEDLINE 22683279
 PUBMED 12799346
 COMMENT Contact: Panopoulou G
 Laboratory 145, dept. Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Ihnestr.63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1235
 Fax: +49 30 8413 1128
 Email: panopoul@molgen.mpg.de
 The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>.
 Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.tzpd.de>).
 PCR Primers
 FORWARD: 5' CCCAGGCTTACACTTATGCTTCGGCTG 3' (M13RSP)
 BACKWARD: 5' GCTATTACGCGACGTGGCAAGGGGATGTG 3' (M13FSP)
 Insert Length: 1 Std Error: 0.00

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Location/Qualifiers

FEATURES
source

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/organism="Branchiostoma floridae"
/mol_type="rRNA"
/db_xref="taxon:7739"
/clone="MPMP531L07115"
/feature_type="whole embryo"
/dev_stage="26 hrs (neutula stage)"
/lab_host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMP531)"
/note="Vector: pSPORT1 (Gibco BRL); Site 1: Sall, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSPORT1 vector using a NotI (5')-pGACTAGTCTAGTCGCGCGCCG (7)15-3' and a Sall (5')-TCGACCCAGCGTCCG-3' adapters (Gibco BRL)."

ORIGIN

Query Match 6.3%; Score 83.2; DB 4; Length 553;
Best Local Similarity 57.8%; Pred. No. 6.9e-08;
Matches 148; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 26 TGAATGCGACAGCGGAGAAAGATTATTCGCCGTTTCGATGCGGAGATACCGGCC 85
DB 287 TGACATGCTATACGCGGAGAGAGTCAACCGCTTCTCAGTGGAGAACTCCAGAA 346
QY 86 GCCAAACGACGCTTCGCGGTGATGCGCAAGACATGTCATGCGCGGCTTTACCT 145
DB 347 GGCTGACAGAGTGGCTGCTCTCATGCTGACGATATATGATGACGCTCTTCACTT 406
QY 146 CTATACATGCTACATCTACTATTCCGGCTGCTGATCTGCTATTTCGACGCAATAG 205
DB 407 CCTATCATTAACCACTACTACTGACCTTCTGACACTTATTCGCTCGACCTAG 466
QY 206 GCATGCTCATTCGACCAACCAAGCCACGATTCGCGCGGCGATCGACGCGCGCAG 265
DB 467 GGTGTGCTGCTACCATGACCAAGTGTCTTCTTATCCAGCCGTTGACGCTGCTCAGC 526
QY 266 CCTGGCGCGCGACCTT 281
DB 527 CCTGAGAGAGGACAT 542

RESULT 8
B2894814 524 bp DNA linear GSS 30-JUL-2003
LOCUS B2894814
DEFINITION Hg4_0102 Hg pUC18 Library Halobaculum gomorrense genomic 5',
genomic survey sequence.

ACCESSION B2894814
VERSION B2894814.1 GI:33345290
KEYWORDS GSS.
SOURCE Halobaculum gomorrense
ORGANISM Halobaculum gomorrense
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobaculum.

REFERENCE 1 (bases 1 to 524)
AUTHORS Goo, Y., Roach, J., Glusman, G., Balliga, N.S., Deutsch, K., Pan, M.,
Dasgupta, S., Ng, W. V. and Hood, L.
TITLE Low-pass sequencing for microbial comparative genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Goo Y
Institute for Systems Biology
1441 North 34th Street, Seattle, WA 98103, USA
Tel: 206 732 1412
Fax: 206 732 1299
Email: ygoosystemsbiology.org
Seq primer: M13 forward
Classes: shotgun.

FEATURES
source 1. .524
Location/Qualifiers
/organism="Halobaculum gomorrense"

/mol_type="genomic DNA"
/strain="ATCC 700876"
/db_xref="taxon:43928"
/clone_lib="Hg pUC18 Library"
/note="Vector: pUC18; Site 1: SmaI; A shotgun library was
constructed from Halobaculum gomorrense genomic DNA using
pUC18/SmaI/BAP plasmid"

ORIGIN

Query Match 5.7%; Score 69.6; DB 8; Length 524;
Best Local Similarity 49.7%; Pred. No. 6.8e-05;
Matches 177; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 764 TCTTGCTTACATACACCGCGCTGAGCGCCACGCTTTCTGCGACCATGTCATGCGCA 823
DB 19 TCGCCGGTACTCTCTGCTGTAACGCTGTCCGCCGACCTTCAGACGCGACGCGC 78
QY 824 GCTTCGATCTGAGAGAAAGACGTGCGCTGATCGCCGCGGCTCGAGTATCAAGC 883
DB 79 AGTGGTCCGGGAGAGAGCCCTCGACGGGTTGCCCCGACCGGACCGGAGCTGCAAG 138
QY 884 CGGCGCGCGCTGCAAGACATCGCCATCGAGCTCAAGAGATGATACCGCGAGTGGAC 943
DB 139 CCGAGAGAGTGCAGCAGACCGGACGACCTCGGATCTACGCGGAGCTCAACGCGAGCGCC 198
QY 944 TGCTGAATGACCGCTCTTCCGCTATGCGCACTCCTTGCGGCTGCTGCGCACTACTAG 1003
DB 199 TGCAAGACTCTTCGACCAACCAATCATCTTGGCGTGAACAGATTGCTCTTCTGCA 258
QY 1004 GTGCGGAGCGCGCTGAGAGTGCAGGAGACATGACAGACCGAGCTGAAGCCGCGATG 1063
DB 259 GCCAGCGCTTACAGCTGAAGCGCGGCGACCTCATCTTCAACGCGGACCGCGGCGTGC 318
QY 1064 TGGTCTCATGAGAGCGATGCTGATGCTGCGGAGAGCGATGCCGCTGCGCGCGC 1119
DB 319 GCGTCTACCGGAGCGCGCGGCTGCTGCTGAGGCGGACACCGTCACTATCGGC 374

RESULT 9
CB656525 722 bp mRNA linear EST 09-APR-2003
LOCUS OSJNEC10P11.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC10P11 5', mRNA sequence.

ACCESSION CB656525
VERSION CB656525.1 GI:29660250
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 722)
AUTHORS Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
TITLE Large-scale identification of ESTs involved in the interaction
JOURNAL between rice and Magnaporthe oryzae
COMMENT Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: P column: 11
Seq primer: gta aac cga cgg cca gtc.

FEATURES
source 1. .722
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mRNA"
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/clone_lib="OSJNBrc"
/notes="Vector: pInscript II KS +; Site 1: EcoRI; Site 2

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ORIGIN

Query Match	5.7%	Score 69.2;	DB 6;	Length 722;
Best Local Similarity	45.0%;	Pred. No. 8.5e-05;		
Matches 260; Conservative	0;	Mismatches 318;	Indels 0;	Gaps 0

Qy	532	GGCGGCGGCGCTGCGCGGCTGCATCAAGCCGGCGTCCGAGCATGAATGGCGAT	591
Db	136	GGCGGCGGCGGCCACGCCCGCGCCGACCAAGCGCGTGTCTTCGCCGTACTGGGACACGGCG	195
Qy	592	GCCACCAACCAATGCGATGATCGCGAGATCGCAATCGTTCCCTTCGTGGAGCTGATG	651
Db	196	AACTGTATCCCGGCGGAGCGTGGCGCGCGTCAAGGGGGGCACTCCCAAGTCAGCGTCATG	255
Qy	652	GACACCTGGAACCTGTTCCAGTCGGGACATCAACACGAGCGCGGCAACATTCGGTCACC	711
Db	256	GTCGGGCTCGGCGGCGGACAGCGTGCAGGACACCGCCAAAGTCTTCTTCCCGGACCTTC	315
Qy	712	AAACCGCATCGTGCATTCGGCGGACATCTCTTTCGCTCAACACTTCCCATGATCTTTCGCG	771
Db	316	GTCACATCGTGGGTGGCCAAAGCGCGCTGCCTCGTCCGGGATATCGACGCTACGCGC	375
Qy	772	TACTACACCGGCTGAGCGGACGCGCTGTTCGTGACCAATGTCATGACCGACGCTCGAC	831
Db	376	CTGACCGGCGTCGACGTGACTACGAGCACTTCAACGACGAGCGCGCGCGCGCTCGAC	435
Qy	832	ATCTGGGAGAAACGTGCGCGTGCATGCGCGCGGCTCGAGCTGATCAAGCGCGGCGCG	891
Db	436	ACGTTCTGTGAGTGCATGGCGCGCTCTCTCAACGAGCTCAAGCGCGGACCCGAACATC	495
Qy	892	CGCTGCAGAGACATCGCCATCGAGCTCAACGAGATGTACCGGAGTGGGACCTGTGTGAG	951
Db	496	ACGACCTTCATCGCGCGCTTGAAGGACCGCGGTGGTGAAGCGTACTACAGCGCGCTGGG	555
Qy	952	TACCGCTCTTCGGCTATGCGCACTCTTCGGCGTGTGTGCACCTACGATGCGGAG	1011
Db	556	CGGCGTACGCGCGGCGTATGCACTCTCAACTTCACAGTTCTACGGCTACGGCGACAAC	615
Qy	1012	GCCGCGGTGAGAGCTGCGGAGGACATCGAACCGAGCTGAAGCCCGGCAATGTTGTTTC	1077
Db	616	ACCACGTCGCGAGCGTACGTATGTTCTTACGACGAGCGCGGCAACTACCCGGGCGCG	675
Qy	1072	ATGGAAGCGATGTGATGCTGCGGAGGAGGACATGCCCG	1109
Db	676	AAGGTGCTCACACGCTTCAAGACCGGCGACGTCGCGG	713

RESULT 10			
CB683938			
LOCUS			
DEFINITION	CB683938	722 bp	mRNA linear EST 09-APR-2003
	OSUNEF12P21.f OSUNEF Oryza sativa (japonica cultivar-group) cDNA clone OSUNEF12P21 5' , mRNA sequence.		
ACCESSION	CB683938		
VERSION	CB683938.1	GI:29687663	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		

REFERENCE
AUTHORS

1 (bases 1 to 722)
Jantaauriyart,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

TITLE	Large-scale identification of ESTs involved in the interaction
JOURNAL	between rice and Magnaporthe grisea
COMMENT	Unpublished (2003)
	Contact: Rod Wing

JOURNAL
COMPTON

COMMENT:

Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088

85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: qta aaa

BACKWARD: oga aac

Plate: 12 row: 6 column: 21

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

seq primer: glr a

FEATURES

source	1. .722
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/organie

 $\text{mol}^{-1} \text{ t y r}^{-1}$

.../culative

/db yref

2010

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clone=
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/issue_

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/dev_sta
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/lab hos

/closure 1

/note="Y

Photo: The

TO : TONY

ORIGIN

Query Match	5.6%	Score 67.6	DB 6	Length 122
Best Local Similarity	44.8%	Pred. No. 0.00019		
Matches 259; Conservative	0	Mismatches 319	Indels 0	Gaps 0

Qy	532	GGGGGGCGCGGCTTGGCGGCGCTGGCCATCAAGGCGCGCTGGCCGAGCATGAGTGGCATC	591
Db	142	GCGGGCGGGCCCAAGCGCGGGCGGACCAAGGGGTGTTCTTGCGGTACTGGGACAGGGCC	201
Qy	592	GCCACCAACCAATGCGATGATCCGCGAGATGCGCCAAATGTTCCCTTCGTGGAGCTGATG	651
Db	202	AACTGTGCCCCGGCGCAAGTGGCCGCGTCAAGGCGGCGACCCCAACGTACAGGTCATG	261
Qy	652	GACACTTGGACTGTGTTCCAGTGGGGCATCAACCGACGGCGGGGACAAATCCGGTCAAC	711
Db	262	GTCGGCTTCGGCGCGCGCAACGCTGACGAGACACCGCCCAAGTCTTCTCCCGACCTCC	321
Qy	712	AACCGCATTCGTGCAATCCGGCGACATCCTTTCGTCAACCTTCGCCAGTATGTTCCGC	771
Db	322	GTCGACTCGTGGGTGGCCAAAGCGGTGGCTTCGCTCCGGCATCATGACGCTTAAGC	381
Qy	772	TACTACACCGCGCTGGAGCGCACGCTGTTCTGGGACCATGTGATGACGACGCTCGAC	831
Db	382	CTGACGCGGCTTCGACGTGCACTACGACATTTCAACACACAGCGGGGGCGGGGTGGAC	441
Qy	832	ATCTGGAGAAAGACGTGGCGGTGATCGCGCGGGCTCGACTGATCAAGCCGGGCGG	891
Db	442	ACGTTGGTGAAGTGCATCGGCGCGCTCTCAACGAGCTCAAGGGCGGGCACCCGAACATC	501
Qy	892	CGCTGCAAGACATTCGCGCATTCGAGCTCAAGGATGTAACCGCGATGGGACCTGCTGAG	951
Db	502	ACCACCTCCATTCGCGCGCTTCGAGGAGCGCGTGGTGCAGGGCTACATCAAGCCGCTGGG	561
Qy	952	TACCGCTCCTTCGGAGTATGCGCACTCCTTCGGCGGTGTGTCGCACTACTACGTCGCGAG	1011
Db	562	CGGCGCTACCGCGCGCTGATCGACCTGTCTCAACTTCCAGTTCTACGGCTACGGGACAAAC	621
Qy	1012	GCCGCGGTGAGGTGCGCGGACGATCGACACCGAGCTGAAGCCCGCATGTGTTCTCC	1071
Db	622	ACCGAGGTGCGGACGTACGTGATGTTCTACGACGAGCAACGGGGGACATCAACGGGGGCGC	681
Qy	1072	ATGAGCCGATGGTATGCTGTCCGAGAGGACATGCCCCG	1109

Db		682AAGGTGCTGCACGACTTCAAGACC9CGCAGCATCACCCG 719
	RESULT 11	CNS0091P 925 bp DNA linear GSS 03-JUN-1999
	LOCUS	CNS0091P/c
	DEFINITION	Drosophila melanogaster genome survey sequence TETJ end of BAC # BACP1916 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
	ACCESSION	CNS0091P
	VERSION	AL053013.1 GI:4934461
	SOURCE	GSS.
	ORGANISM	Drosophila melanogaster (fruit fly)
	REFERENCE	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
	AUTHORS	1 (bases 1 to 925) Genoscope.
	TITLE	Direct Submission
	JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
	COMMENT	Determination of this BAC-end and sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
	FEATURES	Location/Qualifiers
	source	1..925 /organism="Drosophila melanogaster" /mol_type="Genomic DNA" /db_xref="taxon:7227" /clone="BACP1916" /clone_1lb="RPCI-98" /note="end : TETJ"
	ORIGIN	
	Query Match	5.2%; Score 63.6; DB 9; Length 925;
	Best Local Similarity	15.5%; Pred. No. 0.0015;
	Matches	55; Conservative 171; Mismatches 125; Indels 3; Gaps 1;
Oy	228	GGCCACGACGATTTCGGCCGCGATGACGCGGCCAGCCGCGCGAGTTGGCGGA 287
Db	915	CSBBCSSSSSMSTSSSNSBRSCSSBSBSTSSMSSSBSSSGSSSSSGTSBACVK 856
Oy	288	CAACATCACTAACACCGACTGGCGCGCGACACAATTTCATCGCGCGCTGCGCACTGAC 347
Db	855	CNASSCGCCCGGMABCMCMSSSSSCGSASARGVKVAAGAGRGGGSGGASMSHSS 796
Oy	348	CACGGGGCCCAAGCGCATTCGCGATGAGTTGCACACGTCAACTTCGACCTTCGGCCCA 407
Db	795	SACBSSSSSCMSASMSASMSASRSRSGGAGAGSASRSRSSSSSSASAGVWSA 736
Oy	408	GCTCGAGAAGCCCA---CCGGGCGTGATTCGTGCACATCAACCGACCCCTGATGTG 464
Db	735	SSSSSSCSSSVSCSSVASMSGSSSSSSSASMSSSSSSSASCSCCTTSSWCGGST 676
Oy	465	GATGCGCACCATCAAGTCTCGAAGACAGAGTGAITTCGCGAAGCGCCCGCTGTG 524
Db	675	ASMSAARSSSSSSSSSSSMSASASSSSSSSSSSSSSSSSGSAAGBSMSGGGSGS 616
Oy	525	TGACGTGGGCGGCGGCGCTGCGCGCTGCCATCAAGCGCGCGCTGCCAGCA 578

RESULT 12	CD869465	712 bp	mRNA	linear	EST 11-JUL-2001
LOCUS	AZ02.111L14F010208	AZ02	Triticum aestivum	CDNA clone	AZ02111L14,
DEFINITION	CD869465				
ACCESSION	CD869465				
VERSION	CD869465.1				
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.				
REFERENCE	1 (bases 1 to 712)				
AUTHORS	Genoplane, a major partnership french program in plant genomics				
TITLE	Unpublished (2003)				
JOURNAL	Contact: Genoplane				
COMMENT	Genoplane 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genoplane' (http://www.genoplane.com and http://genoplane-info.infobiogen.fr). location/Qualifiers 1..712 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="recital1" /db_xref="taxon:4565" /clone="AZ02111L14" /issue_type="root" /clone_id="AZ02"				
FEATURES					
source					
ORIGIN					
Query Match	5.0%; Score 60.8; DB 6; Length 712;				
Best Local Similarity	44.2%; Pred. No. 0.006;				
Matches 251; Conservative	0; Mismatches 317; Indels 0; Gaps 0;				
Db	550 GCTGCATCAAGCGCGCGTGCAGCAGCATGAACTGCGCATGCGCACCACCAATGCGATG 609				
Db	107 GCCGCGCTCCACGCGCGCATCTCAACAGTGCCTGCTGAGCCCGTCCCGAGCGGAC 166				
Qy	610 ATCCGCGAGATGCGCAATGTTTCCCTTGTGTGAGCTGATGACACTGGAAGCTGTTC 669				
Db	167 GCGGTGTTTACCCGCTCTGTCGCGCGCTGCGCCCGCGGAGCGCGCGCTGTCAGTGGCC 226				
Qy	670 CAGTCGGGACATCAACATCGAGCGGCGGACAAATCCGCTACCAACCGCATGTCATATCC 729				
Db	227 ACCTGAGGCGCGAGGAGGACGAGGATGCGGCGCACTCTGTCGCTGTGCGCGAGCC 286				
Qy	730 GGCACATCTCTTTCGCTCAACACCTTCCGATGATCTTTCGCTTACTACACCGCGCTGAG 789				
Db	287 GAGCGGGCGCTCGAGGGGCACTGCTCGAGCGGCTGCGCGCGCTTCGAGCGCCGCTGCAC 346				
Qy	790 CGCAGCGCTTTCTTCGACCACTGTGTGATGAGCGCCAGCTTCGACATCTGGAGAAAGAGT 849				
Db	347 CACCTCAAGGCTCTTCCCTTACCAAGCAACTACTCTCGGCTGGGCGAGCTGGAACACCG 406				
Qy	850 GCGGTGATGCGCGCGGAGCTCGAGCTATCAAGCGCGGCGCGCGCTCGCAAGAGATGCGC 909				
Db	407 CTGCTGTCCGCGACGCGCGGAGCACTGCGCTGCGCGCGCGCTGCTGCTGCTGCTGCTG 466				
Qy	910 ATCCAGCTCAACGAGATGATCCGCGAGTGGAGCTGTGTAAGTACCGCTCTTTCGCTAT 969				
Db	467 TCGGCTTCCTGCGCGCTCAAGGCGCTCTGCTGCGCGCGCGCGCACATGCGCGAGCGCG 526				
Qy	970 GAGCATCTCTTTCGCGCTGTGTGCTGCTACTACGATGCGAGCGCGCGCGCTGGAAGCTGCG 1029				

Db 527 GTGACTGCTTCGACCGGTGCGGGCGGCGCAAGAGCGGCGTGTCTCCG 586
 Qy 1030 GAGACATCGACACCGAGCTGAAAGCCCGCATGTGTCTTCATGAGCCGATGTGATG 1089
 Db 587 GGGAGACGACACCGCGCGGTGGCGCGCGCATGTGTTCGCAAGCGGACGTGAGTGG 646
 Qy 1090 CTGCGGAGGACATGCGCGGTGGCGGCG 1117
 Db 647 CTGACGACGAGCTCGCGCTTACGACG 674

RESULT 13
 CB659172 812 bp mRNA linear EST 09-APR-2003
 LOCUS OSJNEC15018.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
 DEFINITION clone OSJNEC15018 5', mRNA sequence.
 ACCESSION CB659172
 VERSION CB659172.1 GI:29662897
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 812) Kudra, D., Dean, R., Soderlund, C., Wang, R. and Wang, G. Jantsuriyarc, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kundra, D., Dean, R., Soderlund, C., Wang, R. and Wang, G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea Unpublished (2003)

JOURNAL
 COMMENT Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 15 row: 0 column: 18
 Seg primer: gta aac cga cgg cca gtc.

FEATURES
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="Nipponbare"
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 /clone="OSJNEC15018"
 /issue_type="Leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSJNEC"
 /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
 Query Match 5.0%; Score 60.8; DB 6; Length 812;
 Best Local Similarity 47.2%; Pred. No. 0.006; Mismatches 207; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

Qy 511 GGGCGCCGCGTGTGTGACGTGCGCGGCGCGCTGCGCGGCTGCATCAAGCGCGCGTG 570
 Db 255 GGAAGAGCGGCGCGCGGTGGCGGTGCGGAGCTGGCGCGCTTTTGAAGCAGCGCGTG 314
 Qy 571 CCGGACATGAATGGCGATCGCCACCAACCAATGCGATGATCCGCGAGATCGCAATG 630
 Db 315 GCGCGCGCGCGCTGTGCGTGGCAATCAAGATGCGCGCGCGCGCGCGCGCGTGCGG 374
 Qy 631 TTCCCTTGTGAGTGTGATGACACCTGACCTGATTCAGTGTGCGCATCAACCGAG 690

Db 375 TCGAGTTCGACGCTGTGAACGCGCGGCGCGAGAGACGATCGGTGTGACGACGCC 434
 Qy 691 GGGCGGCAATTCGGTCAACCGCATGTGCAATCCGGGACATCTTTTGGCTCAAC 750
 Db 435 GCGGTCTAGCGCGCTGACCAAGTTCGAGTGAACGGCTGTCCGACCTCGAGTCC 494
 Qy 751 ACCCTCCGATGATCTTCCGCTACTACACCGCGCTGAGACGCGAGCTGTTCGACAT 810
 Db 495 CGGAGAACATCAGATCAATCACTTCACTACCGTGGCAAGCTCAAGCAAGCTGACGG 554
 Qy 811 GTGATGACGCCAGCCTGCATCTGGAGAAAGACGTGCGCTGCATGCGCGGGCTC 870
 Db 555 TTGAGTACGCGGACCAAGTGTGAGAGTGTATCCGACGCTGAGAGGAGGCAACAC 614
 Qy 871 GAGCTGATCAAGCGCGCGCGCGCTGCAAGGA 902
 Db 615 AAGGCGATGTGTGTCTGTCTCAACAGCCAGAA 646

RESULT 14
 AUI62766 604 bp mRNA linear EST 03-APR-2002
 LOCUS AUI62766 Rice mature leaf Oryza sativa (japonica cultivar-group)
 DEFINITION cDNA clone S21656, mRNA sequence.
 ACCESSION AUI62766
 VERSION AUI62766.1 GI:11026165
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 604) Sasaki, T. and Yamamoto, K. Rice cDNA from mature leaf (2000)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agricultural Resources
 Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abr.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/PROJECT="RGP"

FEATURES
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
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 /clone="S21656"
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ORIGIN
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 Best Local Similarity 44.8%; Pred. No. 0.005; Mismatches 285; Indels 0; Gaps 0;
 Matches 231; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

Qy 634 CCCTTCGTGAGCTGTGAGACCTGAGACCTGTGCTTCACTCGGCGCATCAACCGAGCG 693
 Db 57 CGCCCATCTGTGTAGAGAGAGTGTGCGGAGTATCCGCTCTCTCTCACTTCGCC 116
 Qy 694 GGGCAATTCGGTCAACCAACCGATCTGCAATCGGAGACATCTTTCGCTGAACACC 753
 Db 117 GGGCGACGCGCGGACCTTACCAATGAGTCTGCGCTCCACCGCTTCTGTGATC 176
 Qy 754 TTCCGATGATCTTGGCTACTTACACCGGCTGAGAGCGACCTGTTCGCAACATGTC 813
 Db 177 CTCTACTGATGGGGGCTGTGACCGCGCGCTTGGCGCTTCTCTCTCTCTCTCTGTC 236
 Qy 814 GATGACGCGAGCTGACATCTGGAGAAAGATGCGCTGATGCGCGCGGCTCGAG 873

Db 237 GTCTCTACAGCGTCTCTGCGCCAGAGCCTCGGCTCGCATGGCGCCGTGCTCATG 236
 QY 874 CTGATCAAGCCGGCGCGCGCTGCAAGACATGCGCATGCAAGATGATACCGC 933
 Db 297 GAGCTCAAGAGGAGGACACCTCTGCTGCTCATCAACATGGTCTTCTCATGCGCGC 356
 QY 934 GATGTGGAGCTGTGAAGTACCGCTCTTGGCTATAGCCATCTCTTGGCGGTCTGTG 993
 Db 357 GGCTACTACGTCCAGCAGCATCCGCCCTCTGTGCGGTGCTCGGTGGCTCACTACAGC 416
 QY 994 CACTACTACGATGCGAGCGCGGCTGAGCTGCGCGAGACATGCAACCGAGCTGAAG 1053
 Db 417 TTCTACTGCTACCGCTCTCTCATGCGCATCAAGTTCGGCGACGCGCCCTCACTAGAC 476
 QY 1054 CCGGCGATGTGTCTTCCATGAGCCGATGTGTATGCTGCGGAGGCGCATGCCGTGCC 1113
 Db 477 TGGGGGCGCGCGCGCGCGCTGCTGCTGCGCGCATCTCCGCGCATCAAGGCGGTGGG 536
 QY 1114 GGGGCGCTATGCGAGCAGCATCTCTGATGTGTGGG 1149
 Db 537 ATCAACAACCACTGGGTGACGCTGCGCATGANG 572

RESULT 15
 CD225047 668 bp mRNA linear EST 21-MAY-2003
 LOCUS CD225047
 DEFINITION CCNA_37_H01.g1_A007 Callus culture/cell suspension Sorghum bicolor
 ACCESSION CD225047
 VERSION CD225047.1 GI:30968481
 KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor

REFERENCE 1 (bases 1 to 668) Cordomer-Pratt, W.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Rathore, K., Eastman, A. and Pratt, L.H.
 An EST database from Sorghum: callus culture and cell suspension unpublished (2003)

TITLE CCNA_37_H01.b1_A007
 JOURNAL Contact: Cordomer-Pratt KM
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

FEATURES
 source
 1..668
 location/Qualifiers
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="RTx430"
 /db_xref="taxon:4558"
 /clone="CCNA_37_H01_A007"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /note="Vector: pME185-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from a mixture of polyA+ RNA from callus culture tissue and cells in suspension culture. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime

DraIII site is CACGCTGTG. 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."
 ORIGIN
 Query Match 5.0%; Score 60.6; DB 6; Length 668;
 Best Local Similarity 47.5%; Pred. No. 0.0066;
 Matches 180; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 171 CGGCTGGCTGTACTGCTATTGGAAGCAAGTACGGCATGTGATGACCAACAAGC 230
 Db 285 CCGCAAGTTCACCAACCGGTGCGCAACAGGACCAAGCCAACTACAGATCACTG 344
 QY 231 CAGGAGATTGGCGCGGATGACGCGCGCAAGCCCTGGCGGAGCTTGGCGCA 290
 Db 345 CACCAACGACTGGGGGCTCTGCTACGTCAGAGTCCCTGCTGCTGCCCAAGTG 404
 QY 291 CATCACTACACGACTGGCGCGCAATTTCTATTCGCGCTGCGCGACGTGACAC 350
 Db 405 CTTGCTTACTGCGCTTACTGCTTCACTTCTGCAATGTGATGATGCGGGACCTC 464
 QY 351 GGGCGCAAGCGCATGCGATGAGTTGACCAAGTCAATCTGACTTCCGCCAGCT 410
 Db 465 GTGCGGCGACCGCGGTTACGCGCGCGCAAGCAACCTTACTTACAGGCAAGAA 524
 QY 411 CGAGAGCCCTTACCGGGCTGCACTTCTGCAATCAACCCAGCCCTGATGTGATGG 470
 Db 525 GAGCGAGACTTCTGCTGCTTCCGACGACCGCTTCCATCAAGCGCGGTCAATGG 584
 QY 471 CACCATCAAGTGTGCTGGAAGACAGAAAGTGAATCCGGAAGGCGCGGTGTGACGT 530
 Db 585 CAACCAACAGCGCGACTCCGGCGGAGACTTCACTGAGTGAAGGCGCTGGGCTACCTT 644
 QY 531 CGGCGCGCGCGCTGCGG 549
 Db 645 CAGCGCGCGCGAGCGGCGG 663

Search completed: November 19, 2004, 19:22:01
 Job time : 4241 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2004, 12:40:45 ; Search time 653 Seconds

(without alignments)
9743.183 Million cell updates/sec

Title: US-10-807-228-2

Perfect score: 1212

Sequence: 1 ATGACTGACGACATGTTGCA.....AACACACCATCATCGCAAC 1212

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210.4	99.9	1212	2	Aat61367 Creatinin
2	1210.4	99.9	1212	2	Aat38807 Creatine
3	1210.4	99.9	1212	2	Aav35699 Stable cr
4	1210.4	99.9	1212	4	Aa814742 Creatine
5	1210.4	99.9	1212	6	Aa199856 Alkaligen
6	1210.4	99.9	1212	6	Aba93696 Creatine
7	1184.8	97.8	1215	2	Aa113291 Creatine
8	981.6	81.0	1215	8	Acc69514 Erwinia s
9	981.6	81.0	1215	8	Acc69519
10	978.4	80.7	1215	8	Acc69515 Mutant Er
11	976.8	80.6	1212	8	Acc69517 Mutant Er
12	976.8	80.6	1212	8	Acc69516 Mutant Er
13	976.8	80.6	1215	8	Acc69518 Mutant Er
14	975.2	80.5	1212	8	Acc69521 Mutant Er
15	973.6	80.3	1212	8	Acc69520 Mutant Er
16	640.2	52.8	1209	2	Aat05502 Thermosta
17	635.6	52.4	1212	1	Aa60274 Sequence
18	634	52.3	1212	1	Aa81271 Sequence
19	563	46.5	1134	1	Aa70877 Sequence
20	456.2	37.6	1233	1	Aa90635 Sequence
21	317.6	26.2	1282	2	Aa66090 Arthrobac

ALIGNMENTS

22	74	6.1	858	11	ABD05567	ABD05567 Pseudomon
23	74	6.1	963	11	ABD05831	ABD05831 Pseudomon
24	74	6.1	1176	11	ABD05710	ABD05710 Pseudomon
25	72.4	6.0	786	10	ADG73350	ADG73350 Pseudomon
26	72.4	6.0	786	10	ADG73352	ADG73352 Pseudomon
27	69.6	5.7	985	6	ABO44816	ABO44816 Oligonucle
28	69.6	5.7	985	6	ABO44817	ABO44817 Oligonucle
29	68.8	5.7	65140	4	AMD17184	AMD17184 Streptomy
30	68.8	5.7	125401	4	AMD17186	AMD17186 Streptomy
31	67.8	5.6	1227	6	ABL61294	ABL61294 N. uniflor
32	66.8	5.5	2712	8	ACA36793	ACA36793 Prokaryot
33	66.8	5.5	110000	6	ABA03041_18	Continuation (19 o
34	66.8	5.5	110000	6	ACC44573	ACC44573 Glucoamyl
35	65.2	5.4	690	3	AA550948	AA550948 Humanised
36	65	5.4	2052	8	ACA23861	ACA23861 Prokaryot
37	64.8	5.3	3157	2	AAV08896	AAV08896 Cellulobios
38	64	5.3	2364	8	ABV74978	ABV74978 Synthetic
39	63.6	5.2	690	6	AAD46285	AAD46285 Anemonia
40	63.6	5.2	2064	2	AAO52638	AAO52638 Streptomy
41	63.6	5.2	9546	12	ADN40876	ADN40876 Plasmid p
42	63.4	5.2	1083	12	ADJ39271	ADJ39271 Plant CDN
43	62.8	5.2	9785	6	ABK91624	ABK91624 Modified
44	62.4	5.1	1294	2	AAZ06824	AAZ06824 Streptomy
45	62.4	5.1	1294	4	AAH74537	AAH74537 Nucleotid

RESULT 1

AAT61367 standard; DNA; 1212 BP.

AAT61367;

17-APR-1997 (first entry)

Creatinine amidinohydroxylase coding sequence.

Thermal stability; creatinine amidinohydroxylase; creatine; sarcosine;

urea; blood; ds.

Alcaligenes faecalis.

JF08308579-A.

26-NOV-1996.

16-MAY-1995; 95JP-00117283.

16-MAY-1995; 95JP-00117283.

(TOYM) TOYORO KK.

WPI; 1997-059698/06.

P-PSDB; AAM11861.

Gene coding for creatinine amidinohydroxylase - used to quantify blood or

urinary creatinine as a disease indicator.

Claim 4; Page 10-11; 12pp; Japanese.

This sequence encodes a thermally stable creatinine amidinohydroxylase which has a low Km value for creatine. The creatinine amidinohydroxylase has the following physicochemical properties: (a) action: converts creatine and water into sarcosine and urea; (b) optimum temp.: 40-45 deg.C; (c) optimum pH: 8.0-9.0; (d) thermal stability: about 50 or less (pH 7.5, 30 mins); (e) stable pH: a pH range of about 4-10; (f) Km value: about 15.2 mM; (g) mol. wt.: about 4300 (SDS-PAGE); and (h) isoelectric point: about 3.5. The creatinine amidinohydroxylase may be used in the quantification of blood or urinary creatinine and creatine as an indicator of various diseases

SQ Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;
 Query Match 99.9%; Score 1210.4; DB 2; Length 1212;
 Best Local Similarity 99.9%; Pred. No. 1.5e-195;
 Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGACGAGAGACATGTTGACGATGAATGACCAACGGGAGAAAGATTATTCGCG 60
 DB 1 ATGACGAGAGACATGTTGACGATGAATGACCAACGGGAGAAAGATTATTCGCG 60
 QY 61 TTTTCGATGCGGAGATGACCGCGCCAAAGAGAGTTGCGGCTGATGCGCAAGAC 120
 DB 61 TTTTCGATGCGGAGATGACCGCGCCAAAGAGAGTTGCGGCTGATGCGCAAGAC 120
 QY 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCACTAATTCCGCTGGCTG 180
 DB 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCACTAATTCCGCTGGCTG 180
 QY 181 TACTGCTATTTGGAGAGCAAGTACGGCATGTCATGACCAACAGCCCAAGAGATT 240
 DB 181 TACTGCTATTTGGAGAGCAAGTACGGCATGTCATGACCAACAGCCCAAGAGATT 240
 QY 241 TCGGCGCGGATGACGCGCGCGAGCCCTGCGCGGAGCTTGGCGCAACATCACTAC 300
 DB 241 TCGGCGCGGATGACGCGCGCGAGCCCTGCGCGGAGCTTGGCGCAACATCACTAC 300
 QY 301 ACCGACTGGCGCGCGACAAATTTCTATGCGCGCGTGGCGCACTGACACGCGCGCAG 360
 DB 301 ACCGACTGGCGCGCGACAAATTTCTATGCGCGCGTGGCGCACTGACACGCGCGCAG 360
 QY 361 CGCATCGGATGAGTTCGACCAACGTCATCTGATTCGCGCGGAGTTCGAGAGAGCC 420
 DB 361 CGCATCGGATGAGTTCGACCAACGTCATCTGATTCGCGCGGAGTTCGAGAGAGCC 420
 QY 421 CTACGCGGCGCTGACTTCTGACATCAGCCCTCGATGATGATGCGCACTCAAG 480
 DB 421 CTACGCGGCGCTGACTTCTGACATCAGCCCTCGATGATGATGCGCACTCAAG 480
 QY 481 TCGCTCGAAGACAGAACTGATTCGCGAAGCGCGCGTGTGATCCTCGCGCGCGCG 540
 DB 481 TCGCTCGAAGACAGAACTGATTCGCGAAGCGCGCGTGTGATCCTCGCGCGCGCG 540
 QY 541 GCGTCGCGGCGCTGACATCAAGCGCGCGCGGAGATGAGTGGCGATCCGCAACCC 600
 DB 541 GCGTCGCGGCGCTGACATCAAGCGCGCGCGGAGATGAGTGGCGATCCGCAACCC 600
 QY 601 AATGCGATGATCCGCGAGATTCGCAAAATGTTCCCTTCGTGAGAGCTGATGACACTGG 660
 DB 601 AATGCGATGATCCGCGAGATTCGCAAAATGTTCCCTTCGTGAGAGCTGATGACACTGG 660
 QY 661 ACCTGCTTCACTCGGCGATCAACACCGAGCGCGGACATCCGCTCAACACCGCATC 720
 DB 661 ACCTGCTTCACTCGGCGATCAACACCGAGCGCGGACATCCGCTCAACACCGCATC 720
 QY 721 GAGCAATCGGCGGACATCTTTCGCTCAACACCTTCGAGTATCTTGGCTACTACACC 780
 DB 721 GAGCAATCGGCGGACATCTTTCGCTCAACACCTTCGAGTATCTTGGCTACTACACC 780
 QY 781 GCGCTGAGAGCGACGCTTTCGCAACATGTCATGACGCGAGCTTCGACATCTTGGAG 840
 DB 781 GCGCTGAGAGCGACGCTTTCGCAACATGTCATGACGCGAGCTTCGACATCTTGGAG 840
 QY 841 AAGAACGTGGCGGTGATGCGCGCGGCTCGAGCTGATCAACCGCGCGCGCTGCAAG 900
 DB 841 AAGAACGTGGCGGTGATGCGCGCGGCTCGAGCTGATCAACCGCGCGCGCTGCAAG 900
 QY 901 GACATCGGATGAGCTCAACAGAGATGACCGCGAGTGGGACCTGTAAGAACGCTCC 960
 DB 901 GACATCGGATGAGCTCAACAGAGATGACCGCGAGTGGGACCTGTAAGAACGCTCC 960
 QY 961 TTGCGCTATGAGCACTCTTTCGCGCTGCTGTCACATAAGTTCGCGAGCGCGCTG 1020
 DB 961 TTGCGCTATGAGCACTCTTTCGCGCTGCTGTCACATAAGTTCGCGAGCGCGCTG 1020

QY 1021 GAGCTGCCGAGAGACATGACACCGAGCTGAAGCCCGCATGCTGCTCCATGAGCCG 1080
 DB 1021 GAGCTGCCGAGAGACATGACACCGAGCTGAAGCCCGCATGCTGCTCCATGAGCCG 1080
 QY 1081 ATGATGATGCTGCGGAGAGGATGCGCGTCCGCGGCTATTCGAGACAGACATCTCTG 1140
 DB 1081 ATGATGATGCTGCGGAGAGGATGCGCGTCCGCGGCTATTCGAGACAGACATCTCTG 1140
 QY 1141 ATCGTCGGGAGAGAGGTCGCGAGAACATCAACCGCTTCCGTTCCGTCGCGAACACAC 1200
 DB 1141 ATCGTCGGGAGAGAGGTCGCGAGAACATCAACCGCTTCCGTTCCGTCGCGAACACAC 1200
 QY 1201 ATCATCCGCAAC 1212
 DB 1201 ATCATCCGCAAC 1212
 RESULT 2
 AAT38807
 ID AAT38807 standard; DNA; 1212 BP.
 AC AAT38807;
 XX
 AC 17-OCT-2003 (revised)
 DT 02-MAR-1998 (first entry)
 XX
 DE Creatine amidinohydrolase gene.
 XX
 KW Creatine amidinohydrolase enzyme; sarcosine; urea; dye; Km; ds.
 XX
 OS Alcaligenes faecalis; - strain T33581 (FERM P-14237).
 XX
 FH Location/Qualifiers
 FT 1..1212
 FT CDS
 FT /tag= a
 FT /product= "Creatine amidinohydrolase"
 FT /transl_except= (pos:433..435,aa:Glu)
 FT /note= "no stop codon given"
 XX
 PN EP790303-A1.
 XX
 PD 20-AUG-1997.
 XX
 PF 13-FEB-1997; 97EP-00102270.
 XX
 PR 13-FEB-1996; 96JP-00025435.
 XX
 PA (TOYM) TOYO BOSEKI KK.
 XX
 PI Sogabe A, Hattori T, Nishiya Y, Kawamura Y;
 XX
 DR WPI; 1997-404731/38.
 DR P-PSDB; AAM22893.
 XX
 PT Creatine amidinohydrolase enzyme with low Km - for use in assay for
 PT Creatine.
 PS
 PS Disclousure; Page 14-15; 21pp; English.
 CC A novel creatine amidinohydrolase enzyme has been developed which
 CC catalyses the reaction of creatine with water to form sarcosine and urea,
 CC is stable at temperatures of up to 50 degrees Celsius (pH 7.5, 30
 CC minutes) and has an optimum temperature of 40-50 degrees Celsius, optimum
 CC pH of 8-9, a Km value for creatine of 3.5-10 mM in a binding assay using
 CC sarcosine oxidase and peroxidase, a molecular weight of 43 kD by SDS-PAGE
 CC and an isoelectric point of 3.5. The present sequence encodes creatine
 CC amidinohydrolase derived from Alcaligenes faecalis strain T33581 (FERM P-
 CC 14237), which is the wild type creatine amidinohydrolase but is mutated in
 CC the present invention. The enzyme can be used to determine creatine in a
 CC sample by measuring the absorbance of a dye formed by reacting the sample
 CC with a reagent, comprising the enzyme, sarcosine oxidase and a
 CC composition for detecting hydrogen peroxide, e.g. for diagnosis of

CC uremia, chronic nephritis, gigantism and tonic muscular dystrophy. The
 CC enzyme has a lower km value than prior art creatine amidinohydrolase (cf.
 CC US 5451520). (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;

Query Match 99.9%; Score 1210.4; DB 2; Length 1212;

Best Local Similarity 99.9%; Pred. No. 1.5e-195; Mismatches 1; Indels 0; Gaps 0;

Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGACTGACGACATGTCGATGTAATGCAACAACGCGAGAAAGATTATTCGCG 60
 Db 1 ATGACTGACGACATGTCGATGTAATGCAACAACGCGAGAAAGATTATTCGCG 60
 Qy 61 TTTTGGATGCCGAATGACCCGCCCAAAGACGTTCCGGCTGGATGGCCAAAG 120
 Db 61 TTTTGGATGCCGAATGACCCGCCCAAAGACGTTCCGGCTGGATGGCCAAAG 120
 Qy 121 AATGTCGATGGGGCGCTGTCACCTTATCACTGATCACTACTATTCGGGCTGG 180
 Db 121 AATGTCGATGGGGCGCTGTCACCTTATCACTGATCACTACTATTCGGGCTGG 180
 Qy 181 TACTGCTATTTCGACGCAAGTACGCGCATGTCATGACCAACAACGCGACGATT 240
 Db 181 TACTGCTATTTCGACGCAAGTACGCGCATGTCATGACCAACAACGCGACGATT 240
 Qy 241 TCGGCGGCGCATGACGCGGCGGAGCCCTGGCGCGGAGCTTGGCGACAATCAG 300
 Db 241 TCGGCGGCGCATGACGCGGCGGAGCCCTGGCGCGGAGCTTGGCGACAATCAG 300
 Qy 301 ACCGATGCGCGCGCGGCAATTTCTATGCGCGCGCGCGCATGACCAACGCGCG 360
 Db 301 ACCGATGCGCGCGCGGCAATTTCTATGCGCGCGCGCGCATGACCAACGCGCG 360
 Qy 361 CGCATGCGGCATGACGATGACCAACGTCATCTGACCTTCCGCGCGCAGCTCGAG 420
 Db 361 CGCATGCGGCATGACGATGACCAACGTCATCTGACCTTCCGCGCGCAGCTCGAG 420
 Qy 421 CTACCGGCGCTGACCTTGTGACATCAGCCAGCCCTGATGATGGATGGCCATCAG 480
 Db 421 CTACCGGCGCTGACCTTGTGACATCAGCCAGCCCTGATGATGGATGGCCATCAG 480
 Qy 481 TCGCTCGAAGAGCAAGACTGATCGCGCAAGGCGCGCGCTGATGATGGCGCGCG 540
 Db 481 TCGCTCGAAGAGCAAGACTGATCGCGCAAGGCGCGCGCTGATGATGGCGCGCG 540
 Qy 541 GCGTCGCGGCGTGCATCAAGGCGCGGCGCGCGCGCGCGCATGAAAGTGGCGCAC 600
 Db 541 GCGTCGCGGCGTGCATCAAGGCGCGGCGCGCGCGCGCGCATGAAAGTGGCGCAC 600
 Qy 601 AATGCGATGATCCGCGGAGATCGCAATGTTCCCTTCTGAGAGCTGATGACACT 660
 Db 601 AATGCGATGATCCGCGGAGATCGCAATGTTCCCTTCTGAGAGCTGATGACACT 660
 Qy 661 ACCGTCGTCAGTCCGCGCATCAACCGCGCGCGCGCATCCGCTGATCCACCGCAT 720
 Db 661 ACCGTCGTCAGTCCGCGCATCAACCGCGCGCGCGCATCCGCTGATCCACCGCAT 720
 Qy 721 GTGCAATCCGCGGACATCCTTTCGCTCAACACCTTCCCGGATGATCTTGGCTACT 780
 Db 721 GTGCAATCCGCGGACATCCTTTCGCTCAACACCTTCCCGGATGATCTTGGCTACT 780
 Qy 781 GCGCTGAGCGCAACGCTGTTCTGACACATGTCATGACCGGACCTTGCATCTGGAG 840
 Db 781 GCGCTGAGCGCAACGCTGTTCTGACACATGTCATGACCGGACCTTGCATCTGGAG 840
 Qy 841 AAGAACGTGCGCTGTCATCGCGCGGCTGCGAGCTGATCAAGCCGCGCGCTGCAAG 900
 Db 841 AAGAACGTGCGCTGTCATCGCGCGGCTGCGAGCTGATCAAGCCGCGCGCTGCAAG 900
 Qy 901 GACATCGGCATGAGCTCAACGAGATGTACCGGATGGAGCTTCTGAATGACGCTCC 960
 Db 901 GACATCGGCATGAGCTCAACGAGATGTACCGGATGGAGCTTCTGAATGACGCTCC 960

Qy 961 TTGCGCTATGCGCACTCTTGGCGCTGTGTCGCACTACTACTACGATCGGAGCGCGCG 1020
 Db 961 TTGCGCTATGCGCACTCTTGGCGCTGTGTCGCACTACTACTACTACGATCGGAGCGCGCG 1020
 Qy 1021 GAGCTGCGCGAGCATGACCAACGAGCTGAAGCCCGCATGATGCTCTCCATGAGCGCG 1080
 Db 1021 GAGCTGCGCGAGCATGACCAACGAGCTGAAGCCCGCATGATGCTCTCCATGAGCGCG 1080
 Qy 1081 ATGTCGATGCTGCGGAGGCGATCCCGGTCGCGCGCTATTCGAGACGACATCTCTG 1140
 Db 1081 ATGTCGATGCTGCGGAGGCGATCCCGGTCGCGCGCTATTCGAGACGACATCTCTG 1140
 Qy 1141 ATGTCGCGGAGAGCGTCCGAGACATCAACCGGCTTCCGCTCGGTCGCGGACACAC 1200
 Db 1141 ATGTCGCGGAGAGCGTCCGAGACATCAACCGGCTTCCGCTCGGTCGCGGACACAC 1200
 Qy 1201 ATCATCCGCAAC 1212
 Db 1201 ATCATCCGCAAC 1212

RESULT 3

ID AAV35699 standard; DNA; 1212 BP.

AAV35699;

16-SEP-1998 (first entry)

Stable creatine amidinohydrazase encoding DNA.

Creatine amidinohydrazase; mutant; stable; enzyme; diagnostic agent; ds.

Alcaligenes faecalis.

Key Location/Qualifiers

FT CDS 1..1212

FT /tag= a

FT /transl_except= (pos:433..435, aa:Glu)

FT /product= "Stable creatine amidinohydrazase"

FT /note= "the stop codon is not indicated"

PR 17-DEC-1996; 96JP-00337027.

PA (TOYM) TOYORO KK.

PA WPI; 1998-421167/36.

DR P-PSDB; AAM61905.

DR New creatine amidino-hydrazase used as diagnostic agent - is more stable in

PT neutral buffer than wild type creatine amidino-hydrazase.

PS Disclosure; Page 11-13; 14pp; Japanese.

CC This DNA encodes a stable creatine amidinohydrazase which is a mutant

CC creatine amidinohydrazase and has improved long-term stability in a neutral

CC buffer compared to wild type creatine amidinohydrazase. A recombinant

CC plasmid containing the stable creatine amidinohydrazase gene can be used to

CC transform a cell for the recombinant production of the enzyme. This

CC stable creatine amidinohydrazase is useful as a diagnostic agent can be

CC produced commercially

CC

Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;

Query Match 99.9%; Score 1210.4; DB 2; Length 1212;

Best Local Similarity 99.9%; Pred. No. 1.5e-195;

Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ATGACTGACGACATGTTGCACTGTATGAAATGGCAACAGCGGAGAAAGATTATTCGCCG 60
Db 1 ATGACTGACGACATGTTGCACTGTATGAAATGGCAACAGCGGAGAAAGATTATTCGCCG 60
OY 61 TTTTGGATGCGGAGATGACCCCGCGCCAAAAGAGAGTTGCGGGCTGGATGGCAAGAC 120
Db 61 TTTTGGATGCGGAGATGACCCCGCGCCAAAAGAGAGTTGCGGGCTGGATGGCAAGAC 120
OY 121 AATGTCATGCGGCGCTGTTCACTTATCACTGATCACTAATTAATTCGGCTGGTG 180
Db 121 AATGTCATGCGGCGCTGTTCACTTATCACTGATCACTAATTAATTCGGCTGGTG 180
OY 181 TACTGCTATTTGGACGCGAAGTACGGCATGTCATGACACAAAGGCCACGACGATT 240
Db 181 TACTGCTATTTGGACGCGAAGTACGGCATGTCATGACACAAAGGCCACGACGATT 240
OY 241 TCGGCGCGGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 241 TCGGCGCGGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
OY 301 ACCGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 301 ACCGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
OY 361 CGCATCGGCGATGAGTTGACCAAGTCAATCTCGACTTCGCGCGCGCGCGCGCGCGCG 420
Db 361 CGCATCGGCGATGAGTTGACCAAGTCAATCTCGACTTCGCGCGCGCGCGCGCGCGCG 420
OY 421 CTACCGGCGCGTGCATCTTGTCGACATCAAGCCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421 CTACCGGCGCGTGCATCTTGTCGACATCAAGCCGCGCGCGCGCGCGCGCGCGCGCGCG 480
OY 481 TCGCTCGAAGAGCAGAACTGATCCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 481 TCGCTCGAAGAGCAGAACTGATCCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
OY 541 GCGTGGCGGCTGCGCATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 541 GCGTGGCGGCTGCGCATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
OY 601 AATGCGATGATCCGCGAGATCGCAATCGTTCCCTTCGTTGAGGAGCTGATGGACACCTGG 660
Db 601 AATGCGATGATCCGCGAGATCGCAATCGTTCCCTTCGTTGAGGAGCTGATGGACACCTGG 660
OY 661 ACTTGGTTCAGTCCGGGATCAACACCGGCGCGCGCAATCCGGTCAACCAACCGCATC 720
Db 661 ACTTGGTTCAGTCCGGGATCAACACCGGCGCGCGCAATCCGGTCAACCAACCGCATC 720
OY 721 GTGCAATCCGGGAGATCTTTCCGTCACACCTTCCGATGATCTTGGGCTACTACACC 780
Db 721 GTGCAATCCGGGAGATCTTTCCGTCACACCTTCCGATGATCTTGGGCTACTACACC 780
OY 781 GCGCTGAGAGCGCAGCTGTTTCGAGACCATGTCATGACGCGAGCCTGCAATCTGGAG 840
Db 781 GCGCTGAGAGCGCAGCTGTTTCGAGACCATGTCATGACGCGAGCCTGCAATCTGGAG 840
OY 841 AAGAACGTGGCGGTCATCGCGCGGCTCGAGCTCAACCCCGGCGCGCGCGCTGCAAG 900
Db 841 AAGAACGTGGCGGTCATCGCGCGGCTCGAGCTCAACCCCGGCGCGCGCGCTGCAAG 900
OY 901 GACATCGGCGATGAGCTCAAGAGATGTAACCGGAGTGGAGCTTCTGAATACCGCTCC 960
Db 901 GACATCGGCGATGAGCTCAAGAGATGTAACCGGAGTGGAGCTTCTGAATACCGCTCC 960
OY 961 TTTGGCTATGCGCACTCTTCCGCGCTGCTGTCACCTACTACGATCGCGAGGCGCGCTG 1020
Db 961 TTTGGCTATGCGCACTCTTCCGCGCTGCTGTCACCTACTACGATCGCGAGGCGCGCTG 1020
OY 1021 GAGCTGCGGAGAGATCGACACCGAGTGAAGCCCGGATGATGATCTTCATGGAGCGG 1080
Db 1021 GAGCTGCGGAGAGATCGACACCGAGTGAAGCCCGGATGATGATCTTCATGGAGCGG 1080

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OY 1081 ATGGTGAATGCTGCGGAGGCGGATGCCGCTGCGCGCGCTATCCGAGCAGACATCCTG 1140
Db 1081 ATGGTGAATGCTGCGGAGGCGGATGCCGCTGCGCGCGCTATCCGAGCAGACATCCTG 1140
OY 1141 ATCGTGGGAGAGACGGTGCAGAGACATCACCGGCTTCCGTTCCGTCGGTCCGAAACACAC 1200
Db 1141 ATCGTGGGAGAGACGGTGCAGAGACATCACCGGCTTCCGTTCCGTCGGTCCGAAACACAC 1200
OY 1201 ATCATCCGCAAC 1212
Db 1201 ATCATCCGCAAC 1212

RESULT 4
AA14742
ID AA14742 standard; DNA; 1212 BP.
XX
AC AA14742;
XX
DT 19-DEC-2001 (first entry)
XX
DE Creatine amidinohydrolase genomic DNA.
XX
KW Creatine amidinohydrolase; water; sarcosine; urea; creatinine; uraemia;
KW chronic nephritis; acute nephritis; tonic muscular dystrophy; giantism;
KW pigment absorbance; ds.
XX
OS Alkaligenes faecalis.
XX
FH Key
FT 1. .1212
FT CDS
FT
FT /*cag= a
FT /product= "A. faecalis creatine amidinohydrolase"
FT /transl_except= (pos:433..435, aa:Glu)
FT /partial
FT /note= "No stop codon"
XX
XX BP1132467-A2.
XX
PD 12-SEP-2001.
XX
PF 13-FEB-1997; 2001EP-00113052.
XX
PR 13-FEB-1996; 96JP-00025435.
XX
PR 13-FEB-1997; 97EP-00102270.
XX
PA (TOYM ) TOYO BOSEKI KK.
XX
PI Sogabe A, Hattori T, Nishiya Y, Kawamura Y;
XX
XX WPI; 2001-612481/71.
XX
DR P-PSDB; AAU08727.
XX
PT New creatine amidinohydrolase, useful as a routine reagent for clinical
PT tests for determining creatine and creatinine in biological samples,
PT particularly useful in diagnosing diseases such as uremia or chronic
PT nephritis.
XX
XX Disclosure; Page 15-16; 21pp; English.
XX
XX The invention relates to Alkaligenes faecalis creatine amidinohydrolase,
XX which catalyzes creatine and water to sarcosine and urea. Creatine
XX amidinohydrolase can be produced by culturing a microorganism producing
XX the protein in a nutrient medium and recovering the protein from the
XX resulting culture. Creatine amidinohydrolase is useful as a routine
XX reagent for clinical tests for determining creatine and creatinine in
XX biological samples. This is particularly useful in diagnosing diseases
XX such as uraemia, chronic nephritis, acute nephritis, giantism and tonic
XX muscular dystrophy. The presence of creatine in a sample can be
XX determined by measuring an absorbance of a pigment produced by the
XX reaction of a reagent containing creatine amidinohydrolase with the
XX sample. This sequence represents genomic DNA encoding Alkaligenes

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CC faecalis creatine amidinohydrolase

XX Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;

Query Match 99.9%; Score 1210.4; DB 4; Length 1212;

Best Local Similarity 99.9%; Pred. No. 1.5e-195;

Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 ATGATGACGACATGTTGACGATGTAATGAGCAACGCGGAGAAAAGATTATTCGCG 60
Db 1 ATGATGACGACATGTTGACGATGTAATGAGCAACGCGGAGAAAAGATTATTCGCG 60
Oy 61 TTTTGGATGCGGATGATACCGCGGCAAAAGAGCTTGGGGTGGATGGCCAAAGAC 120
Db 61 TTTTGGATGCGGATGATACCGCGGCAAAAGAGCTTGGGGTGGATGGCCAAAGAC 120
Oy 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCACTAATTCGCGTGGCTG 180
Db 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCACTAATTCGCGTGGCTG 180
Oy 181 TACTGCTATTTGACGCAAGTACGCGCATGTCATGACCAACACAGCCACGACGATT 240
Db 181 TACTGCTATTTGACGCAAGTACGCGCATGTCATGACCAACACAGCCACGACGATT 240
Oy 241 TCGGCGGCGCATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 TCGGCGGCGCATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Oy 301 ACCGACTGCGGCGGCGGCAATTTCTATGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 ACCGACTGCGGCGGCGGCAATTTCTATGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 360
Oy 361 CGCATCGGCGCATGACGTCGACGACGATCTGCACTTCCGCGCGGCGGCGGCGGCGG 420
Db 361 CGCATCGGCGCATGACGTCGACGACGATCTGCACTTCCGCGCGGCGGCGGCGGCGG 420
Oy 421 CTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 CTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Oy 481 TCGCTCGAAGAGCAGAGCTGATCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 481 TCGCTCGAAGAGCAGAGCTGATCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Oy 541 GCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 541 GCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Oy 601 AATGCGATGATCGCGGAGATCGCCAAATCGTTCCCTTCGTGAGCTGATGACACCTGG 660
Db 601 AATGCGATGATCGCGGAGATCGCCAAATCGTTCCCTTCGTGAGCTGATGACACCTGG 660
Oy 661 ACCGTGGTTCCAGTCCGGGATCAACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 ACCGTGGTTCCAGTCCGGGATCAACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Oy 721 GTGCAATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 721 GTGCAATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Oy 781 GCGCTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 781 GCGCTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Oy 841 AAGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
Db 841 AAGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
Oy 901 GACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
Db 901 GACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
Oy 961 TTGGGCTATGCGCACTCTTGGGCGGCTGTGCGCACTACTACGATCGGCGGCGGCGG 1020

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Db 961 TTTGGGCTATGCGCACTCTTGGGCGGCTGTGCGCACTACTACGATCGGCGGCGGCGG 1020
Oy 1021 GAGCTGCGCGGAGCATGACACCGAGCTGAAGCCCGGCGGATGATGATTCATGAGCGG 1080
Db 1021 GAGCTGCGCGGAGCATGACACCGAGCTGAAGCCCGGCGGATGATGATTCATGAGCGG 1080
Oy 1081 ATGATGATGCTGCGGAGGAGGAGATGCGCGGTCGCGGCGGCTATTCGAGACAGACTCTG 1140
Db 1081 ATGATGATGCTGCGGAGGAGGAGATGCGCGGTCGCGGCGGCTATTCGAGACAGACTCTG 1140
Oy 1141 ATCGTCGGGAGGAGCGGTCGCGGAGAACTACCGGCTTCCGCTTCGTCGAGACACACC 1200
Db 1141 ATCGTCGGGAGGAGCGGTCGCGGAGAACTACCGGCTTCCGCTTCGTCGAGACACACC 1200
Oy 1201 ATCATTCGCGCAC 1212
Db 1201 ATCATTCGCGCAC 1212

```

RESULT 5

AA199856
ID AA199856 standard; DNA; 1212 BP.

AC AA199856;
XX
XX 07-AUG-2003 (revised)
DT 28-JAN-2002 (first entry)

Alkaligenes faecalis creatineamidinohydrolase encoding DNA.

Alkaligenes faecalis; TE3581; FERM P14237; creatineamidinohydrolase; ds.

Alcaligenes faecalis.

Key Location/Qualifiers

FT CDS 1..1212

FT /tag= a

FT /transl_except= (pos:433..435,aa:Glu)

FT /product= "creatineamidinohydrolase"

FT /partial

FT /note= "CDS lacks a stop codon"

XX JP2001252088-A.

XX 18-SEP-2001.

XX 16-MAY-1995; 2001JP-00051054.

XX 16-MAY-1995; 95JP-00117283.

XX (TOYM) TOYOBOKK.

XX WPI: 2002-003140/01.

XX P-PSDB; AAM51471.

XX A gene encoding creatineamidinohydrolase.

XX Claim 4; Page 10; 11pp; Japanese.

XX The invention relates to Alcaligenes faecalis TE3581 (FERM P-14237)

XX CC creatineamidinohydrolase and the encoding gene. The gene can be used for

XX CC the commercial preparation of creatineamidinohydrolase. (Updated on 07-

XX AUG-2003 to correct OS field.)

XX Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;

XX Query Match 99.9%; Score 1210.4; DB 6; Length 1212;

XX Best Local Similarity 99.9%; Pred. No. 1.5e-195;

XX Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ATGATGACGACATGTTGACGATGTAATGAGCAACGCGGAGAAAAGATTATTCGCGG 60

Db 1 ATGACTGACGACATGTTTGCAGTGTGAAATGGCAACAAGCGGCGAAGAAAGTATTTCCCG 60
Qy 61 TTTTCCGATGCCGATGATGACCCCGCCCAAAAGAGCTTGGCGCTGGATGGCCAGAAC 120
Db 61 TTTTCCGATGCCGATGATGACCCCGCCCAAAAGAGCTTGGCGCTGGATGGCCAGAAC 120
Qy 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCAACTACTATTCGCGCTGGCTG 180
Db 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCAACTACTATTCGCGCTGGCTG 180
Qy 181 TACTGCTATTTCCGACGCAAGTACGCGATGATTCGACCAACAACGCGCAGACGATT 240
Db 181 TACTGCTATTTCCGACGCAAGTACGCGATGATTCGACCAACAACGCGCAGACGATT 240
Qy 241 TCGGCGCGGATTCGACGCGCGCGCGCGCTGGCGCGCTTCCGCGCAACATCACTAC 300
Db 241 TCGGCGCGGATTCGACGCGCGCGCGCGCTGGCGCGCTTCCGCGCAACATCACTAC 300
Qy 301 ACCGACTGGCGCGCGCGCAATTTCTATCGCGCGTGGCCAGCTGACCAAGCGCGCCAG 360
Db 301 ACCGACTGGCGCGCGCGCAATTTCTATCGCGCGTGGCCAGCTGACCAAGCGCGCCAG 360
Qy 361 CGCATCGGCGATCGAGTTTCAACAGTCAATCTGACTTCCGCGCGAGCTCGAGAACCC 420
Db 361 CGCATCGGCGATCGAGTTTCAACAGTCAATCTGACTTCCGCGCGAGCTCGAGAACCC 420
Qy 421 CTACCGGCGCTCGACTTCTGTCGATCAGCCAGCTCGATGATGATGCGCAGCATCAAG 480
Db 421 CTACCGGCGCTCGACTTCTGTCGATCAGCCAGCTCGATGATGATGCGCAGCATCAAG 480
Qy 481 TCGCTGGAAGAGAGAGAGTATCCGCGAGAGGCGCGCGTGTGATGATGCGCGCGCGCG 540
Db 481 TCGCTGGAAGAGAGAGAGTATCCGCGAGAGGCGCGCGTGTGATGATGCGCGCGCGCG 540
Qy 541 GCCTGCGCGGCTGCCATCAAGGCGCGGCGCGCGAGATGAAGTGGCGATCGCCACACC 600
Db 541 GCCTGCGCGGCTGCCATCAAGGCGCGGCGCGCGAGATGAAGTGGCGATCGCCACACC 600
Qy 601 AATGCGATGATCCGCGAGATCGCCAAATGTTCCCTTCTGAGAGCTGATGACACCTGG 660
Db 601 AATGCGATGATCCGCGAGATCGCCAAATGTTCCCTTCTGAGAGCTGATGACACCTGG 660
Qy 661 ACCTGCTTCAGTCCGCGCATCAACGCGCGCGCGCAATCCGCGTCAACGCGCATC 720
Db 661 ACCTGCTTCAGTCCGCGCATCAACGCGCGCGCGCAATCCGCGTCAACGCGCATC 720
Qy 721 GTGCAATCCGCGGACATCTTTTGTCTCAACACCTTCCGATGATCTTGGCTACTACCC 780
Db 721 GTGCAATCCGCGGACATCTTTTGTCTCAACACCTTCCGATGATCTTGGCTACTACCC 780
Qy 781 GCGCTGGAGCGGCGCTGTTCTGGACATGTCGATGAGCGCCAGCTTCGACATCTGGAG 840
Db 781 GCGCTGGAGCGGCGCTGTTCTGGACATGTCGATGAGCGCCAGCTTCGACATCTGGAG 840
Qy 841 AAGAACTGGGCGTGTGATCGCGCGGCGCTGAGCTATCAAGCGCGCGCGCGCTCAAG 900
Db 841 AAGAACTGGGCGTGTGATCGCGCGGCGCTGAGCTATCAAGCGCGCGCGCGCTCAAG 900
Qy 901 GACATGCGCATCGAGTCAAGATGTAACGCGATGGGAGCTTGTGAAGTACCGCTCC 960
Db 901 GACATGCGCATCGAGTCAAGATGTAACGCGATGGGAGCTTGTGAAGTACCGCTCC 960
Qy 961 TTGCGCTATGCGCACTCTTCCGCGCTGTGTGCTGCTACTACGCTGCGAGCGCGCTG 1020
Db 961 TTGCGCTATGCGCACTCTTCCGCGCTGTGTGCTGCTACTACGCTGCGAGCGCGCTG 1020
Qy 1021 GAGCTGCGGAGGACATCGACGAGCTGAAGCGCGGATGGTGGTTCATGAGCGCG 1080
Db 1021 GAGCTGCGGAGGACATCGACGAGCTGAAGCGCGGATGGTGGTTCATGAGCGCG 1080
Qy 1081 ATGCTGATGCTGCGGAGGCGATGCCGCTGCGCGGCTATGCGAGCAGCATCTG 1140
Db 1081 ATGCTGATGCTGCGGAGGCGATGCCGCTGCGCGGCTATGCGAGCAGCATCTG 1140

Qy 1141 ATGCTGAGGAGGACGCTGCCGAGAACATCACCGGCTTCCGTTCCGTCGGACACACC 1200
Db 1141 ATGCTGAGGAGGACGCTGCCGAGAACATCACCGGCTTCCGTTCCGTCGGACACACC 1200
Qy 1201 ATCATCCGCAC 1212
Db 1201 ATCATCCGCAC 1212
RESULT 6
ABA93696
ID ABA93696 standard; DNA; 1212 BP.
XX ABA93696;
XX
XX 29-APR-2002 (first entry)
XX
DE Creatine amidinohydrazase encoding DNA SEQ ID NO:2.
XX
KW Creatine amidinohydrazase; enzyme; mutant; stable; clinical diagnosis;
XX gene; de.
XX
OS Alcaligenes faecalis.
XX
FH Key Location/Qualifiers
FT CDS 1..1212
FT /*tag= a
FT /product= "creatine amidinohydrazase"
FT /transl_except= (pos:433..435,aa:Glu)
FT /note= "no stop codon given"
XX
PN JP2001346594-A.
XX
XX 18-DEC-2001.
XX
XX 17-DEC-1996; 2001JP-00121708.
XX
XX 17-DEC-1996; 96JP-00337027.
XX
XX (TOYOBO KK.
XX
DR WPI: 2002-145187/19.
XX P-PSDB; ABB05660.
XX
XX
PT Mutant creatine amidinohydrazase for use in clinical diagnosis has long-
PS term stability in a neutral buffer solution.
XX
XX Claim 12; Page 12-13; 15pp; Japanese.
XX
XX The present invention describes a stable mutant creatine amidinohydrazase
XX having a long-term stability in a neutral buffer solution. Also described
XX are: (1) a creatine amidinohydrazase gene encoding the above stable
XX creatine amidinohydrazase; (2) a gene encoding a mutant creatine
XX amidinohydrazase having a long-term stability in a neutral buffer solution
XX compared to wild type creatine amidinohydrazase, in which at least one gene
XX among those found in a fully defined 1212 nucleotide sequence (the
XX present sequence) is replaced by another gene; (3) a recombinant plasmid
XX containing a gene encoding the above creatine amidinohydrazase; (4) a cell
XX transformed by the above plasmid; and (5) a method for the preparation of
XX a stable creatine amidinohydrazase in which the above cell is cultured in a
XX medium and creatine amidinohydrazase is collected. The creatine
XX amidinohydrazase is useful as a clinical diagnosing agent
XX
SQ Sequence 1212 BP; 244 A; 400 C; 358 G; 210 T; 0 U; 0 Other;
Query Match 99.9%; Score 1210.4; DB 6; Length 1212;
Best Local Similarity 99.9%; Pred. No. 1.5e-195;
Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACTGACGACATGTTTGCAGTGTGAAATGGCAACAAGCGGCGAAGAAAGTATTTCCCG 60
Db 1 ATGACTGACGACATGTTTGCAGTGTGAAATGGCAACAAGCGGCGAAGAAAGTATTTCCCG 60

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QY 61 TTTTGGATGCGGAGATGACCCGCGCGCAAAAGAGTTTCGCGGTGATGAGCAAGAAC 120
DB 61 TTTTGGATGCGGAGATGACCCGCGCGCAAAAGAGTTTCGCGGTGATGAGCAAGAAC 120
QY 121 AATGTGATGCGGCGGTGTTCACTTATCACTGATCAACTATATCCGGCTGGCTG 180
DB 121 AATGTGATGCGGCGGTGTTCACTTATCACTGATCAACTATATCCGGCTGGCTG 180
QY 181 TACTGCTATTTGCGAGCAAGTACGCGATGATGATGACCAACAACGCGCAAGATTT 240
DB 181 TACTGCTATTTGCGAGCAAGTACGCGATGATGATGACCAACAACGCGCAAGATTT 240
QY 241 TGGGCGCGGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 TGGGCGCGGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 ACCGACTGCGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 ACCGACTGCGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 CGCATGCGGATGAGTTGACCAAGTCAATCTTCACTTCCGCGCGCGCGCGCGCGCG 420
DB 361 CGCATGCGGATGAGTTGACCAAGTCAATCTTCACTTCCGCGCGCGCGCGCGCGCG 420
QY 421 CTACCGGCGGTGACTTCTGTCGATCAACGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 CTACCGGCGGTGACTTCTGTCGATCAACGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 TCGCTCGAAGAGCAGAAAGTGAATCCGGAAGGCGCGCGGTGATGATGATGATGATG 540
DB 481 TCGCTCGAAGAGCAGAAAGTGAATCCGGAAGGCGCGCGGTGATGATGATGATGATG 540
QY 541 GCGTGGCGCGCTGCCATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
DB 541 GCGTGGCGCGCTGCCATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 601 AATGCGATGATCCGCGAGATCCGCAATGCTTCCCTTGTGAGAGTGAATGCAACCTG 660
DB 601 AATGCGATGATCCGCGAGATCCGCAATGCTTCCCTTGTGAGAGTGAATGCAACCTG 660
QY 661 ACCTGCTTCAGTCCGCGCATCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 ACCTGCTTCAGTCCGCGCATCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GTGCAATCCGCGGACATCTTTCGCTCAACACCTTCCGATGATCTTCCGCTACTAC 780
DB 721 GTGCAATCCGCGGACATCTTTCGCTCAACACCTTCCGATGATCTTCCGCTACTAC 780
QY 781 GCGCTGAGGCGGACGCTTTCGCGGACGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GCGCTGAGGCGGACGCTTTCGCGGACGATGATGATGATGATGATGATGATGATGAT 840
QY 841 AAGAAAGTGGCGGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 841 AAGAAAGTGGCGGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 901 GACATCGCCATGAGCTCAAGAGATGTAACGCGAGTGGAGCTGTGTAAGTACGCTTC 960
DB 901 GACATCGCCATGAGCTCAAGAGATGTAACGCGAGTGGAGCTGTGTAAGTACGCTTC 960
QY 961 TTTGCGCTATGCGCACTCTTTCGCGGTGCTGTGCTCACTTACGCTGCGCAAGCGCG 1020
DB 961 TTTGCGCTATGCGCACTCTTTCGCGGTGCTGTGCTCACTTACGCTGCGCAAGCGCG 1020
QY 1021 GAGCTGCGGAGGAGATGACACCGAGCTGAAGCCCGGATGATGATGATGATGATG 1080
DB 1021 GAGCTGCGGAGGAGATGACACCGAGCTGAAGCCCGGATGATGATGATGATGATG 1080
QY 1081 AATGATGATGCTGCGGAGGAGATGCGCGGTGCGCGGCTATGCGAGCAGACATCTCT 1140
DB 1081 AATGATGATGCTGCGGAGGAGATGCGCGGTGCGCGGCTATGCGAGCAGACATCTCT 1140

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QY 1141 ATCGTCGGGAGGAGCGGTGCGGAGAACATCACCGGCTTCCGTTGCGTCCGGAACAC 1200
DB 1141 ATCGTCGGGAGGAGCGGTGCGGAGAACATCACCGGCTTCCGTTGCGTCCGGAACAC 1200
QY 1201 ATCATCCGCAAC 1212
DB 1201 ATCATCCGCAAC 1212

RESULT 7
AAT13291
ID AAT13291 standard; DNA; 1215 BP.
XX
AC AAT13291;
XX
DT 16-OCT-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
DE Creatine amidinohydrolyase.
XX
KW Creatine amidinohydrolyase; CAH; kidney; disease; Alcaligenes; de.
XX
OS Alcaligenes sp.; KS-85 PERM BP-4487.
XX
FH Key Location/Qualifiers
FT misc_difference 319..321
FT FT /tag=a
FT FT /transl_except= 319..321; aa:asn
XX
PN DE1936506-A1.
XX
PD 04-APR-1996.
XX
PF 29-SEP-1995; 95DE-01036506.
XX
PR 29-SEP-1994; 94JP-00235737.
XX
PA (KIRK ) KIRKMAN CORP.
XX
PI Furukawa K, Ichikawa T, Suzuki M, Koyama Y;
XX
DR WPI: 1996-180805/19.
XX
DR P-PSDB; AAR94463.
XX
FT DNA encoding creatine amidinohydrolyase - useful for quantification of
PT creatine to, e.g. diagnose kidney disease.
XX
PS Claim 1; Page 9-11; 18pp; German.
XX
CC CAH is used for quantification of creatine, e.g. to diagnose kidney
CC disease by measuring creatine content of serum or urine. CAH DNA can be
CC inserted into host cells for the prodn. of CAH. CAH can now be produced
CC efficiently without having to add creatine to the culture medium.
CC (updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1215 BP; 247 A; 398 C; 357 G; 213 T; 0 U; 0 Other;

Query Match 97.8%; Score 1184.8; DB 2; Length 1215;
Best Local Similarity 98.6%; Pred. No. 3-2e-191;
Matches 1195; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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QY 181 TACGCTATTTCGAGCGCAAGTACGGCATGTCATCGACCAACAACGCCAGAGATT 240
DB 181 TACTGCTATTTCGAGCGCAAGTACGGCATGTCATCGACCAACAACGCCAGCGATT 240
QY 241 TCGGCGCGGATCGACCGCGCGCAGCCCTGGCGCGCGAGCTTCGCGCAACAATCACTAC 300
DB 241 TCGGCGCGGATCGACCGCGCGCAGCCCTGGCGCGCGAGCTTCGCGCAACAATCACTAC 300
QY 301 ACCGACTGGCGCGCGCAATTTCTATCGCGCGCGTGGCCAGCTGACCAAGCGCGCCAA 360
DB 301 ACCGACTGGCGCGCGCAATTTCTATCGCGCGCGTGGCCAGCTGACCAAGCGCGCCAA 360
QY 361 CGCATCGGATCGAGTTCGACCAAGTATCTGATCTGCGCGCGCGAGTGAAGGCC 420
DB 361 CGCATCGGATCGAGTTCGACCAAGTATCTGATCTGCGCGCGCGAGTGAAGGCC 420
QY 421 CTACCGGCGGCTGACTTCGTGCAATCGACCGAGCCCTCGATGATGATGCGCACATCAAG 480
DB 421 CTACCGGCGGCTGAGTTCGTGCAATCGACCGAGCCCTCGATGATGATGCGCACATCAAG 480
QY 481 TCGCTCGAAGAGCAAGAGTATCCGCGAAGCGCGCGCGTGTGTGACGTTCGCGCGCG 540
DB 481 TCGCTCGAAGAGCAAGAGTATCCGCGAAGCGCGCGCGTGTGTGACGTTCGCGCGCG 540
QY 541 GCCTGCGCGGCTGSCATCAAGAGCGCGCGCGCGAGCATGAATGGCGATCGCCACAC 600
DB 541 GCCTGCGCGGCTGCCATCAAGAGCGCGCGCGCGAGCATGAATGGCGATCGCCACAC 600
QY 601 AATGCGATGATCCGCGAGATCGCCAAATCGTTCCTTCGTGAGCTGATGACACCTGG 660
DB 601 AATGCGATGATCCGCGAGATCGCCAAATCGTTCCTTCGTGAGCTGATGACACCTGG 660
QY 661 ACCTGCTTCCAGTTCGGGCGATCAACACCGAGCGCGCGCAATCCGCTCACCAACCGCAT 720
DB 661 ACCTGCTTCCAGTTCGGGCGATCAACACCGAGCGCGCGCAATCCGCTCACCAACCGCAT 720
QY 721 GTCGCAATCCGCGAGATCCCTTCGTCAACACCTTCGCTGATCTTCGCTGCTACTAC 780
DB 721 GTCGCAATCCGCGAGATCCCTTCGTCAACACCTTCGCTGATCTTCGCTGCTACTAC 780
QY 781 GCGCTGAGAGCGACGCTGTTCTGCGACATGTCATGACCGCGAGCTTCGACATCTGGAG 840
DB 781 GCGCTGAGAGCGACGCTGTTCTGCGACATGTCATGACCGCGAGCTTCGACATCTGGAG 840
QY 841 AAGAAGCTGCGCGCTGCAATCGCCGCGGCTGAGCTGATCAAGCGCGCGCGCTGCAAG 900
DB 841 AAGAAGCTGCGCGCTGCAATCGCCGCGGCTGAGCTGATCAAGCGCGCGCGCTGCAAG 900
QY 901 GACATGCGCATCGAGCTCAACGAGATGTAACCGGAGTGGGAGCTGCTGAAGTACCGCTCC 960
DB 901 GACATGCGCATCGAGCTCAACGAGATGTAACCGGAGTGGGAGCTGCTGAAGTACCGCTCC 960
QY 961 TTCGCTATGCGCACTCTTCGCGCGTGTGTCACATCACTGATCGGTGCGAGCGCGCGT 1020
DB 961 TTCGCTATGCGCACTCTTCGCGCGTGTGTCACATCACTGATCGGTGCGAGCGCGCGT 1020
QY 1021 GAGCTCGCGGAGCATTCGACACCGAGCTGAAACCGCGCATGTGTGCTTCATGAGCGCG 1080
DB 1021 GAGCTCGCGGAGCATTCGACACCGAGCTGAAACCGCGCATGTGTGCTTCATGAGCGCG 1080
QY 1081 ATGGTATGCTGCGGAGGAGCATGCCGGTGGCGGCGGATGAGCGAGCATCTCTG 1140
DB 1081 ATGGTATGCTGCGGAGGAGCATGCCGGTGGCGGCGGATGAGCGAGCATCTCTG 1140
QY 1141 ATGCTGCGGAGGAGCATGCGAGAAATCAACCGGCTTCCTTCGCTCGGAGCAACAC 1200
DB 1141 ATGCTGCGGAGGAGCATGCGAGAAATCAACCGGCTTCCTTCGCTCGGAGCAACAC 1200
QY 1201 ATCATTCGCAAC 1212
DB 1201 ATCATTCGCAAC 1212

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RESULT 8
ACC69514
ID ACC69514 standard; DNA; 1215 BP.
XX
AC ACC69514;
XX
DT 21-JUL-2003 (first entry)
XX
DE Erwinia sp. (DSM 97-934) creatinase encoding DNA SEQ ID NO:1.
XX
KW Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3;
KW Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism;
KW chronic nephritis; acute nephritis; tonic muscular dystrophy; gene; ds.
XX
OS Erwinia sp.
XX
Key Location/Qualifiers
FT CDS 1..1215
FT /tag= a
FT /EC_number= "3.5.3.3"
FT /product= "creatinase"
XX
PN EP1298213-A1.
XX
PD 02-APR-2003.
XX
PF 17-SEP-2002; 2002EP-00020793.
XX
PR 20-SEP-2001; 2001EP-00121780.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Shao Z, Schmuck R, Kratzsch P, Kenkies J, Weisser H;
XX
DR WPI; 2003-383834/37.
XX
DR P-PSDB; ABR43467.
XX
PT New variant of an Erwinia-type creatinase modified relative to a wild-
PT type creatinase having creatinase activity, useful for determining
PT creatinine and/or creatine concentration in a sample.
XX
PS Disclosure; Page 15-17; 51pp; English.
XX
CC The present invention describes a variant of an Erwinia-type creatinase
CC (I) modified relative to a wild-type creatinase having creatinase
CC activity. The variant comprises at least one amino acid substitution at a
CC position of the fully defined 404 amino acid sequence given in ABR43467;
CC these are selected from N130, M203, I278, I1304 and F395. Creatinase has
CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.
CC Also described is a reagent (II) for determining creatine comprising the
CC Erwinia-type creatinase variant. The variant is useful for determining
CC creatinine and/or creatine concentration in a sample. Measuring
CC creatinine and creatine are useful for diagnosing uraemia, chronic
CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some
CC other related diseases. The mutant enzymes have improved stability, lower
CC conductivity and/or lower Km-values for creatine: they are much better
CC suited to detection methods for creatine. The present sequence encodes
CC Erwinia sp. (DSM 97-934) wild-type creatinase from the present invention
XX
SQ Sequence 1215 BP; 242 A; 392 C; 358 G; 223 T; 0 U; 0 Other;
Query Match 81.0%; Score 981.6; DB 8; Length 1215;
Best Local Similarity 88.1%; Pred. No. 6; 5e-157;
Matches 1068; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
QY 1 ATGACTGACGACATGTTGAGCTGATGAATGGACACCGGAGGAAAGATTATTCGCCG 60
DB 1 ATGACTGACGACATGTTGAGCTGATGAATGGACACATGTGTGAAGAAATATTCGCC 60
QY 61 TTTTCGATGCGGAGATGACCGCGCGCAACGACGTTGCGGCTGATGCGCAAGAAC 120
DB 61 TTTTCGATGCGGAGATGACCGCGCGCAAGTACGTGCGGCGCTGATGCGCGCAAGAAC 120

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OY	121	AATGTCGAGCGCGCGCTGTTCACTCTTTATCACTGATCAACAATCAATTCGGCTGAGTC	180
DB	121	GAGCTGACGCTGCGCTGTTCACTCTTATCATTTGATCAATTAATCACTTGGAATTCCTG	180
OY	181	TACTGCTATTTCCGACGCAAGTACGGCATGTCATCGACACACAAACGCCACGATTC	240
DB	181	TACTGCTATTTCCGCGCGCAAAATACGGCATGTCATCGACACCAATCCACGACATTC	240
OY	241	TGGGCGCGGATATGACGCGCGGCCAGCCCTTGCGCCGACGTTGGGCGCAACAATCACCTTAC	300
DB	241	TGGGCGCGGATGATGATGGCCGCTCAGCCCTTGCGCGCGGATTCGGCGCAACAATCACTTAT	300
OY	301	ACCGACTGGCGCGCGACAACTTTCTATCGCGCGCTGCGCAGGTGACACGCGGCGCGAAG	360
DB	301	ACGGACTGGCGCGCGCGACAACTTTCTATCAGCGCGCTGCGCMACTCACCCCGCGCGAAG	360
OY	361	CGCATTCGCGATCGAGTTGTCGACCACTGTAATCTTCGACTTCGCGCGCAGCTCGAAGAGCC	420
DB	361	CGCATTCGCGATCGAGTTGATCAGCGTAACCTTGTACCTTCGCGCGCACGCTCGAAGAGCG	420
OY	421	CTACCGGCGGATGAGACTTGGTCGACATCAACCGACCGCTCGATGATGATGCGACCAATCAAG	480
DB	421	CTGCCCCGAGCTGAGTTCTGTCGATTCGGTCAACCGTCGATGATGATGCGACCGGCTAAG	480
OY	481	TGCGTCGAAGAGACAGAGCTGATTCGCGAAGGCGCGCGGTGTGACGTCGCGCGCGCG	540
DB	481	TGCGTCGAAGAGACAGAGCTGATTCGCGAAGGCGCGCGGTGTCGATCTGCGACGTCGCGGTCG	540
OY	541	GCGTCGCGGCGCTGCCATCAAGGCGCGCGCGCGCGCGACATGAAGTGGCATTCGCGCACCC	600
DB	541	GCGTCGCGGCGCGCGCTGCCATCAAGGCGCGCGCGCGCGCGACAGAGTGGCATTCGCGCACAC	600
OY	601	AATGCGATGATTCGCGAGATTCGCCAAATGCTTCCCTTGCGGAGCTGATGACACTGCG	660
DB	601	AATGCGATGATTCGCGAGATTCGCCAAATGCTTCCCTTGCGGAGCTGATGACACTGCG	660
OY	661	ACCTGCTTCCAGTCCGAGCATCAACACCGAGCGCGCACAAATCCGATCAACACCGCATTC	720
DB	661	ACCTGCTTCCAGTCCGAGCATCAACACCGAGCGCGCACAAATCCGATGACCAACCGCATTC	720
OY	721	GTGCAATCCGCGGAGATACCTTTGCGTCMAACAACCTTCCCGGATGATCTTGCGGCTATCAACCC	780
DB	721	GTGCAATCCGCGGAGATACCTTGCGCTCAACAACGTTCCCATATATCTTGCGGCTATCAACCG	780
OY	781	GCGCTGAGCGCACGCTGTTCTTGCGACCATGTCGATGACGCGACGCTCGACATCTTGCGAG	840
DB	781	GCGCTGAGCGCAACGCTGTTCTTGCGACCATGTCGATGACGCGCTTGACATCTTGCGAG	840
OY	841	AAGAACTGCGCGCTGTCATCGCGCGGCGCTCGAGCTGATCAAGCCGCGCGCGCTGCGAG	900
DB	841	AAGAACTGCGCGCTGTCACCGCGCGCGCGCTCGAATCATCAACCGCGGCTGCGCTGCGAG	900
OY	901	GACATTCGCGCATGAGCTCAACGAGATGTAACCGCGAGTGGGAACCTGTAAGTACCGCTCC	960
DB	901	GATATTCGCGCATGAACTCAACGAGATGTAACCGCGAGTGGGAATCTGCTGAATGACCGCTCC	960
OY	961	TTCCGCTATGCGCACTCTTCGCGCGTGTGTCGCACTACAGATCGCGAGGCGCGGCGTG	1020
DB	961	TTCCGCTATCGGCGCACTCTTCGCGCGTGTCTTCCACTACAGGCGCGGCGGCGGCGTG	1020
OY	1021	GAGCTGCGCGAGGAGATCGACACCGAGCTGAAGCCCGGATGATGATGCTTCCCATGGAAGCG	1080
DB	1021	GAACTGCGCGAGGAGATCGATACCGTGTGCGACGCCCGGATGATGATGCTTCCCATGGAAGCG	1080
OY	1081	ATGTGATGCTCCCGGAGGCGCATGCGCGGTGCGCGCGCTATTCGCGACGACGACATCTCGT	1140
DB	1081	ATGTGATGTTGCGCAAGAGCGCTCCCGCGCGGCGGCTACCGGAGGACGACATCTCGT	1140
OY	1141	ATCGTTCGCGGAGAGATGCTGCGGAGAAATCACTACCGGCTTCCGTTTGGTTCGGAACAACCC	1200
DB	1141	ATCGTTCGCGGAGAGATGCTGCGGAGAAATCACTACCGGATTCCTTCTGGGCTGGAAGACAAC	1200

Query Match	81.04;	Score 981.6;	DB 8;	Length 1215;
Best Local Similarity	88.15;	Pred. No. 6.5e-157;		
Matches 1066;	Conservative 0;	Mismatches 144;	Indels 0;	Gaps 0;

QY 1 ATGACTGACGACATGTTTGCATGATGAAATGGCAACAAGCGGAGAAAGTTATTGCGCG 60
 Db 1 ATACGACGACATGTTGACGTGATGAAATGGCAACAATGATGAAAGAAATTTCCCCC 60
 QY 61 TTTTGGATGCGGATGACCCGCGCAAAAGCAACCTTGGCGCTGATGCGCAAGAC 120
 Db 61 TTTTCCGATGCCAGATGACGCCCGCGCAAGTGAAGCTGGCGGCTGATGCGCAAGAC 120
 QY 121 AATGTCGATGCGGCGCTGTTCACTCTTATCACTGATCAACTATTCCGCGTGGCTG 180
 Db 121 GACGTGACGCTGCGCTGTTCACTCTTATCACTGATCAACTACTCTGATGGACTG 180
 QY 181 TACTGCTATTTCGAGCGCAAGTACGATGCTATGACCAACAACGCGCAAGAGATT 240
 Db 181 TACTGCTATTTCGAGCGCAAAATGCGATGCTATGACCAAGACATGCGCAAGACATC 240
 QY 241 TCGGCGGCGCATGACGCGCGCGCAAGCCCTGCGCGCGGAGCTTTCGCGCAACATCACTAC 300
 Db 241 TCGGCGGCGCATGACGCGCGCTGAGCCCTGCGCGCGGAGCTTTCGCGCAACATCACTAT 300
 QY 301 ACCGACTGCGCGCGCGCAAAATTTCTATCGCGCGCTGCGCGCAAGCTGACCAAGCGCGCAAG 360
 Db 301 ACCGACTGCGCGCGCGCAAACTTCTACCAAGCGCGCTGCGCGCAACTCAACCGCGCGCAAG 360
 QY 361 CGGATGCGCATGCAAGTTTCCACACGTCATCTGCACTTCCGCGCGCAAGCTGCGCAAGCC 420
 Db 361 CGGATGCGATTCAGATTCAGATTCAGTGAAGCTTTCGCGCGCAAGCTGCGCAAGCGG 420
 QY 421 CTACCGGCGCGTCACTTCTGTCGACATCAGCCAGCCCTGATGTCGATGTCGACATCAAG 480
 Db 421 CTGCGCGCGCTCAAGTTCTGTCGATTCGTCGACACCTGATGTCGATGTCGCGCGCTCAAG 480
 QY 481 TCGCTCGAAGAGAGAGAGCTGATCCGCGAAGCGCGCGCTGTCGATCGTCCGCGCGCG 540
 Db 481 TCGCTCGAAGAGAGAGAGCTGATCCGCGAAGCGCGCGCTGTCGATCGTCCGCGCGCG 540
 QY 541 GCGTGGCGGCTGCGCATCAAGGCGCGCGCGCGCGCGCGCTGTCGATCGTCCGCGCGCG 600
 Db 541 GCGTGGCGGCTGCGCATCAAGGCGCGCGCGCGCGCGCGCTGTCGATCGTCCGCGCAAC 600
 QY 601 AATGCGATGATCCGCGAGATCCGCAATCGTTCCCTTGGTGGAGTGAATGACACTG 660
 Db 601 AATGCGATGATCCGCGAGATCCGCAATCGTTCCCTTGGTGGAGTGAATGACACTG 660
 QY 661 ACCTGTTCAGTCCGCGCATCAACACGAGCGCGCGCAACATCCGCTCAACACCGCATC 720
 Db 661 ACCTGTTCAGTCCGCGCATCAACACGAGCGCGCGCAACATCCGCTCAACACCGCATC 720
 QY 721 GTGCGATCCGCGGACATCTTGTGCTCAACACTTCCCGATGATCTTGGCTACTACAC 780
 Db 721 GTGCGATCCGCGGACATCTTGTGCTCAACACTTCCCGATGATCTTGGCTACTACAC 780
 QY 781 GCGCTGGAGCGCGCTGTTCTGCGACATGTCGATGAGCGCGCTGCAACATCTGGAG 840
 Db 781 GCGCTGGAGCGCGCTGTTCTGCTGACACGTCGATGAGTCGAGCTTGAACACTGGAG 840
 QY 841 AAGAACGTGCGCTGTCATGCGCGCGCTGTCGATGATCAAGCGCGCGCGCTGCAAG 900
 Db 841 AAGAACGTGCGCTGTCATGCGCGCGCTGTCGATGATCAAGCGCGCGCGCTGCAAG 900
 QY 901 GACATGCGCATGAGTCAACGAGATGTCACGAGATGGGACTGCTGAAGTACCGCTCC 960
 Db 901 GATATGCGCATGAGTCAACGAGATGTCACGAGATGGGATGCTGAAGTACCGCTCC 960
 QY 961 TTGCGGCTATGCGCACTCTTCCGCGCTGTCGATGATCAAGCGCTGCGAGCGCGCTG 1020
 Db 961 TTGCGGCTATGCGCACTCTTCCGCGCTGCTCTCCACTATCAAGCGCGCGAGCGCGCTG 1020
 QY 1021 GAGCTGCGGAGAGACATCAACGAGCTGAAGCGCGCGAGTGTCTTCATGAGCGG 1080
 Db 1021 GAACTGCGGAGAGACATCAACGAGCTGAAGCGCGCGAGTGTGTCTTCATGAGCGG 1080
 QY 1081 ATGTGTATGCTGCGGAGGAGATGCGCGGATGCGCGGCGCTATGCGAGACACATCTCTG 1140

Db 1081 ATGTGTATGCTGCGAAGGCGCTCTCCGCGCGCGCTACCGGAGACACATCTCTG 1140
 QY 1141 ATGTCGCGGAGAGAGGTCGCCGAGAACATCACGCGCTTCCGTCGTCGCGAACAACACC 1200
 Db 1141 ATGTCGCGGAGAGAGGCGCGAGAACATTTACGGAATCCCTTGGCGCTGAGACCAAC 1200
 QY 1201 ATCATCCGCAAC 1212
 Db 1201 ATCATCCGCAAC 1212
 RESULT 10
 ACC69515
 ID ACC69515 standard; DNA; 1215 BP.
 XX
 AC ACC69515;
 XX
 DT 21-JUL-2003 (first entry)
 XX
 DE Mutant Erwinia creatinase CTIm24 encoding DNA SEQ ID NO:9.
 XX
 KW Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3;
 XX Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism;
 KW chronic nephritis; acute nephritis; tonic muscular dystrophy; mutant;
 KW gene; ds.
 XX
 OS Erwinia sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1..1215
 FT /*tag= a
 FT /EC number= "3.5.3.3"
 CDS /product= "creatinase mutant CTIm24"
 XX
 PN EP1298213-A1.
 PD 02-APR-2003.
 XX
 PF 17-SEP-2002; 2002EP-00020793.
 XX
 PR 20-SEP-2001; 2001EP-00121780.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Shao Z, Schmuck R, Kratzsch P, Kenkies J, Weisner H;
 XX WPI, 2003-383834/37.
 DR P-PSDB; ABR43474.
 XX
 PT New variant of an Erwinia-type creatinase modified relative to a wild-
 PT type creatinase having creatine activity, useful for determining
 PT creatinine and/or creatine concentration in a sample.
 XX
 PS Example 4; Page 20-21; 51dp; English.
 XX
 CC The present invention describes a variant of an Erwinia-type creatinase
 CC (I) modified relative to a wild-type creatinase having creatinase
 CC activity. The variant comprises at least one amino acid substitution at a
 CC position of the fully defined 404 amino acid sequence given in ABR43467;
 CC these are selected from N130, M203, I278, I1304 and P395. Creatinase has
 CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.
 CC Also described is a reagent (II) for determining creatine comprising the
 CC Erwinia-type creatinase variant. The variant is useful for determining
 CC creatinine and/or creatine concentration in a sample. Measuring
 CC creatinine and creatine are useful for diagnosing uraemia, chronic
 CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some
 CC other related diseases. The mutant enzymes have improved stability, lower
 CC conductivity and/or lower Km-values for creatine; they are much better
 CC suited to detection methods for creatine. The present sequence encodes a
 CC mutant Erwinia creatinase from the present invention

XX Sequence 1215 BP; 241 A; 393 C; 359 G; 222 T; 0 U; 0 Other;
 SQ Query Match 80.7%; Score 978.4; DB 8; Length 1215;
 Best Local Similarity 88.0%; Pred. No. 2.2e-156;
 Matches 1066; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 1 ATGACGACGACGATGTCAGCGATGAAATGGCACAAAGGCGAGAAAGTTATTTGGCG 60
 DB 1 ATGACGACGACGATGTCAGCGATGAAATGGCACAAATGGAAGAAATATTCCTCC 60
 QY 61 TTTTCGATGCCAGATGACCCCGCGCAAAACGAGTTTCGCGCTGATGAGCGCAAG 120
 DB 61 TTTTCGATGCCAGATGACCGCGCGCAAGTGAAGTGGCGGCTGATGAGCGCAAG 120
 QY 121 AATGTCATGAGCGCGCTGTTCACTCTTATCATGCACTCACTAATTCGCTGCTG 180
 DB 121 GACGTGACGCTGCGCTGTTCACTCTTATCATGCACTCACTAATTCGCTGCTG 180
 QY 181 TACTGCTATTTGGAGCAAGTACGGCATGTCATGACCAACAAACCGCAGAGATT 240
 DB 181 TACTGCTATTTGGAGCAAGTACGGCATGTCATGACCAACAAACCGCAGAGATT 240
 QY 241 TCGGCGCGCATCGACCGCGCGCAGCCCTGCGCGCGAGCTTCGCGCGCAACATCACTAC 300
 DB 241 TCGGCGCGCATCGATGCGCGCTGAGCCCTGCGCGCGCTGAGCTTCGCGCGCAACATCACTAT 300
 QY 301 ACCGACTGCGCGCGCACAATTTCTATCGCGCGCTGCGCGCACTGACCAAGCGCGCAAG 360
 DB 301 ACCGACTGCGCGCGCGCACACTTTCTACAGCGCGCTGCGCGCACTGACCCCGCGCGCAAG 360
 QY 361 CGCATGCGATGATTCGACCAACGTCATCTTCGCGCGCGCGCGCGCGCGCGCGCG 420
 DB 361 CGCATGCGATGATTCGACCAACGTCATCTTCGCGCGCGCGCGCGCGCGCGCGCG 420
 QY 421 CTACCGCGCGCTGACTTCCTGCAATCAGCGCGCGCTGATGATGCGCGCATCAAG 480
 DB 421 CTGCGCGCGCTGAGTTCTGCAATTCGCGCGCGCTGATGATGCGCGCATCAAG 480
 QY 481 TCGCTCGAAGACGAGCTGATCGCGCGCGCGCGCGCGCGCTGATGATGCGCGCG 540
 DB 481 TCGCTCGAAGACGAGCTGATCGCGCGCGCGCGCGCGCGCTGATGATGCGCGCG 540
 QY 541 GCCTGCGCGCTGCGCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
 DB 541 GCCTGCGCGCTGCGCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
 QY 601 AATGCGATGATCGCGCGAGATCGCGCAATGCTTCCTGCTGATGATGACACCTG 660
 DB 601 AATGCGATGATCGCGCGAGATCGCGCAATGCTTCCTGCTGATGATGACACCTG 660
 QY 661 ACTGCTTCAGTCGCGCATCAACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCATC 720
 DB 661 ACTGCTTCAGTCGCGCATCAACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCATC 720
 QY 721 GTGCAATCGCGCGCATCTTTGCTGCAACACTTCCTGATGATCTTCGCTGATCAAC 780
 DB 721 GTGCAATCGCGCGCATCTTTGCTGCAACACTTCCTGATGATCTTCGCTGATCAAC 780
 QY 781 GGGCTGAGAGCGCGCTGCTGCGACATGTCATGACGCGCGCTGCACTCTGAGAG 840
 DB 781 GGGCTGAGAGCGCGCTGCTGCTGTCGACACGTCGACGATGACGCTTGAACCTTGA 840
 QY 841 AAGAACGTGCGCGCATGCGCGCGCTGCGAGCTGATCAAGCGCGCGCGCGCGCGCG 900
 DB 841 AAGAACGTGCGCGCATGCGCGCGCTGCGAGCTGATCAAGCGCGCGCGCGCGCGCG 900
 QY 901 GACATGCGCATGAGCTCAACGAGATGTCACCGAGTGGAGCTGCTGATGATGCGCTCC 960
 DB 901 GATATGCGCATGAGCTCAACGAGATGTCACCGAGTGGAGTCTGCTGATGATGCGCTCC 960
 QY 961 TTCGGTATGCGCACTCTTCGCGCTGCTGCTGCACTCACTGCGCGCGCGCGCGT 1020
 DB 961 TTCGGTATGCGCACTCTTCGCGCTGCTGCTGCACTCACTGCGCGCGCGCGCGT 1020

DB 961 TTCGGTATGCGCACTCTTCGCGCTGCTGCTGCACTCACTGCGCGCGCGCGCGT 1020
 QY 1021 GAGCTGCGCGAGACATGCAACCGAGCTGAAAGCCCGGATGATGCTTCATGAGCGG 1080
 DB 1021 GAGCTGCGCGAGACATGCAATCCGCTGCGAGCCCGGATGATGCTTCATGAGCGG 1080
 QY 1081 ATGTCATGCTGCTCGGAGGCGATGCGCGGCTGCGCGCTATGCGAGACGACATCTG 1140
 DB 1081 ATGTCATGCTGCTCGGAGGCGATGCGCGGCTGCGCGCTATGCGAGACGACATCTG 1140
 QY 1141 ATGTCGCGGAGACGCGTCCGAGAACATCACCGCTTCCTGCTGCGGAAACACACC 1200
 DB 1141 ATGTCGCGGAGAGACGCGCGCAGAGAACATTAACCGATTCCTTCGCGCTGAGCAAC 1200
 QY 1201 ATCATCCGCAAC 1212
 DB 1201 ATCATCCGCAAC 1212

RESULT 11
 ACC69517
 ID ACC69517 standard; DNA; 1212 BP.
 XX
 AC ACC69517;
 XX
 DT 21-JUL-2003 (first entry)
 XX
 DE Mutant Erwinia creatinase CT2m10 encoding DNA SEQ ID NO:13.
 XX
 KW Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3;
 KW Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism;
 KW chronic nephritis; acute nephritis; tonic muscular dystrophy; mutant;
 KW gene; de.
 XX
 OS Erwinia sp.
 OS Synthetic.
 OS
 FT Key Location/Qualifiers
 FT CDS 1..1212
 FT /*tag= a
 FT /partial
 FT /EC number= "3.5.3.3"
 FT /product= "creatinase mutant CT2m10"
 FT /note= "no stop codon given"
 FT
 PN EP1298213-A1.
 XX
 PD 02-APR-2003.
 PD
 PF 17-SEP-2002; 2002EP-00020793.
 PF
 PR 20-SEP-2001; 2001EP-00121780.
 PR
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Shao Z, Schmuck R, Kratzsch P, Kenkies J, Weisser H;
 XX
 DR WPI; 2003-383834/37.
 DR P-PSDB; ABR43476.
 DR
 PT New variant of an Erwinia-type creatinase modified relative to a wild-
 PT type creatinase having creatinase activity, useful for determining
 PT creatinine and/or creatine concentration in a sample.
 XX
 PS Example 4; Page 26-28; 51pp; English.
 XX
 CC The present invention describes a variant of an Erwinia-type creatinase
 CC (1) modified relative to a wild-type creatinase having creatinase
 CC activity. The variant comprises at least one amino acid substitution at a
 CC position of the fully defined 404 amino acid sequence given in ABR43467;
 CC these are selected from N130, M203, I278, I1304 and P395. Creatinase has
 CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.

CC Also described is a reagent (II) for determining creatine comprising the
 CC Erwinia-type creatinase variant. The variant is useful for determining
 CC creatinine and/or creatine concentration in a sample. Measuring
 CC creatinine and/or creatine are useful for diagnosing uremia, chronic
 CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some
 CC other related diseases. The mutant enzymes have improved stability, lower
 CC conductivity and/or lower Km-values for creatine; they are much better
 CC suited to detection methods for creatine. The present sequence encodes a
 CC mutant Erwinia creatinase from the present invention
 CC
 XX

Sequence 1212 BP; 240 A; 394 C; 358 G; 220 T; 0 U; 0 Other;

Query Match 80.6%; Score 976.8; DB 8; Length 1212;
 Best Local Similarity 87.9%; Pred. No. 4.2e-156;

Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 ATGACTGACGACATGTTGCAAGTGAATGGAACACGCGAGAAAGATTATTCGCCG 60
 DB 1 ATGACTGACGACATGTTGCAAGTGAATGGAACATGTGAAAGAAATATTCGCCG 60
 QY 61 TTTTCGATCCGAGATGACCCGCCCAAAAGACGCTGCGCTGGATGGCCAAAGAC 120
 DB 61 TTTTCGATCCGAGATGACCCGCCCAAGATGACGCTGCGCTGGATGGCCAAAGAC 120
 QY 121 AATGTGATGCGGCGCTTACCTCTTATCAGTCATCACTACTATTCCGGCTGGCTG 180
 DB 121 GAGCTGACGCGTGGCTGTTCACTCTTATCAGTCATCACTACTATTCCGGCTGGCTG 180
 QY 181 TACTGCTATTTCCGACGCAAGTACGCGATGATCGACACCAACACGCGACGAGATT 240
 DB 181 TACTGCTATTTCCGACGCAAGTACGCGATGATCGACACCAACACGCGACGAGATT 240
 QY 241 TCGGCGGCGATCGACGCGCGCCGACGCTGCGCGCCGACGCTTGGCGCAACATCAGCTAC 300
 DB 241 TCGGCGGCGATCGACGCGCGCCGACGCTGCGCGCCGACGCTTGGCGCAACATCAGCTAC 300
 QY 301 ACCGACTGGCGCGCGCAATTTCTATCGCGCGTGGCGAGCTGACCAAGCGCGCGCAAG 360
 DB 301 ACCGACTGGCGCGCGCAATTTCTATCGCGCGTGGCGAGCTGACCAAGCGCGCGCAAG 360
 QY 361 CGGATCGGCGATCGAGTTGCAACAGTCAATCTGCACTTCCGCGCGACGCTCGAGGAAGCC 420
 DB 361 CGGATCGGCGATCGAGTTGCAACAGTCAATCTGCACTTCCGCGCGACGCTCGAGGAAGCC 420
 QY 421 CTACCGGCGCTGCACTTCTGTCATCAGTCAAGCCCTCTGATGTGATGGCGACATCAAG 480
 DB 421 CTACCGGCGCTGCACTTCTGTCATCAGTCAAGCCCTCTGATGTGATGGCGACATCAAG 480
 QY 481 TCGCTCGAAGAGCAGAACTGATCGCGAAGGCGCGCGCTGTGTGACGTGCGCGCGCG 540
 DB 481 TCGCTCGAAGAGCAGAACTGATCGCGAAGGCGCGCGCTGTGTGACGTGCGCGCGCG 540
 QY 541 GCCTGCGGCTGCGCATCAAGGCGCGGTGCGCGAGATGAAGTGGCGATCGCCACACC 600
 DB 541 GCCTGCGGCTGCGCATCAAGGCGCGGTGCGCGAGATGAAGTGGCGATCGCCACACC 600
 QY 601 AATGCGATGATCCGCGAGATCGCCAAATGTTTCCCTTGTGAGAGCTGATGACACTGG 660
 DB 601 AATGCGATGATCCGCGAGATCGCCAAATGTTTCCCTTGTGAGAGCTGATGACACTGG 660
 QY 661 ACCTGTTCCAGTCGCGGATCAACACGCGCGCGCAATTCGGGTGACCAACCGCATC 720
 DB 661 ACCTGTTCCAGTCGCGGATCAACACGCGCGCGCAATTCGGGTGACCAACCGCATC 720
 QY 721 GTGCAATCCGCGGACATCTTTGCTCAACACCTTCCGATGATCTTGGCTACTACAC 780
 DB 721 GTGCAATCCGCGGACATCTTTGCTCAACACCTTCCGATGATCTTGGCTACTACAC 780
 QY 781 GCGCTGAGAGCGACGCTTGTTCGACATGTGATGACGCGCTCGACATCTGAGAG 840
 DB 781 GCGCTGAGAGCGACGCTTGTTCGACATGTGATGACGCGCTCGACATCTGAGAG 840
 QY 841 AAGAACGTGCGGTGATCGCGCGGCGCTGAGCTGATCAAGCGCGCGCGCTGCAAG 900

DB 841 AAGAACGTGCGGTGATCGCGCGGCGCTGAGCTGATCAAGCGCGGCTGCGCTGCAAG 900
 QY 901 GACATCGCATCGAGTCAACAGATGTACCGCGAGTGGAGCTGTGAAATACGCTCC 960
 DB 901 GATATCGCATCGAATCAACAGATGTACCGCGAGTGGAGCTGTGAAATACGCTCC 960
 QY 961 TTGCGTATGCGCTCTTCCGCGCTGTGTGTCACCTACTAGGTGTCGAGCGCGCGCTG 1020
 DB 961 TTGCGTATGCGCTCTTCCGCGCTGTGTGTCACCTACTAGGTGTCGAGCGCGCGCTG 1020
 QY 1021 GAGCTGCGGAGACATCGACACCGAGCTGAAGCCCGGAGTGTGCTTCCATGAGACCG 1080
 DB 1021 GAGCTGCGGAGACATCGATACCGCTGTCGACGCCCGGATGTGCTTCCATGAGACCG 1080
 QY 1081 ATGTGATGCTCCGAGAGCGATGCGCGCGTGGCGGCTATCGCGAGACGACATCTTG 1140
 DB 1081 ATGTGATGCTCCGAGAGCGATGCGCGCGTGGCGGCTATCGCGAGACGACATCTTG 1140
 QY 1141 ATCGTGGGAGAGAGCGTGGCGCGCAACATCAACGCGCTTCCGCTGCGGAAACACAC 1200
 DB 1141 ATCGTGGGAGAGAGCGGCGCGCAACATTAACCGGATTCCTCGGCGCTGACACAC 1200
 QY 1201 ATCATCCGCAAC 1212
 DB 1201 ATCATCCGCAAC 1212

RESULT 12
 ACC69516
 ID ACC69516 standard; DNA; 1212 BP.
 XX
 AC ACC69516;
 XX
 DT 21-JUL-2003 (first entry)
 XX
 DE Mutant Erwinia creatinase CT2m9 encoding DNA SEQ ID NO:11.
 XX
 KW Erwinia, creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3;
 KW Erwinia-type creatinase; creatine; creatinine; uremia; gigantism;
 KW chronic nephritis; acute nephritis; tonic muscular dystrophy; mutant;
 KW gene; de.
 OS Erwinia sp.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT CDS 1..1212
 FT /*tag= a
 FT /partial
 FT /EC_number= "3.5.3.3"
 FT /product= "creatinase mutant CT2m9"
 FT /note= "no stop codon given"
 XX
 EP1298213-A1.
 PD 02-APR-2003.
 PF 17-SEP-2002; 2002EP-00020793.
 XX
 PR 20-SEP-2001; 2001EP-00121780.
 XX
 PA (HOPF) ROCHE DIAGNOSTICS GMBH.
 PA (HOPF) HOPFMANN LA ROCHE & CO AG F.
 PI Shao Z, Schwuck R, Kratzsch P, Kenkles J, Weisner H;
 DR MPI: 2003-383834/37.
 DR P-PSDB; ABR43475.
 XX
 PT New variant of an Erwinia-type creatinase modified relative to a wild-
 PT type creatinase having creatinase activity, useful for determining
 PT creatinine and/or creatine concentration in a sample.

XX Example 4; Page 23-25; Sipp; English.

CC The present invention describes a variant of an Erwinia-type creatinase
 CC (I) modified relative to a wild-type creatinase having creatinase
 CC activity. The variant comprises at least one amino acid substitution at a
 CC position of the fully defined 404 amino acid sequence given in ABR4467.
 CC These are selected from N130, M203, I278, I1304 and P395. Creatinase has
 CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.
 CC Also described is a reagent (II) for determining creatine comprising the
 CC Erwinia-type creatinase variant. The variant is useful for determining
 CC creatinine and/or creatine concentration in a sample. Measuring
 CC creatinine and/or creatine are useful for diagnosing uraemia, chronic
 CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some
 CC other related diseases. The mutant enzymes have improved stability, lower
 CC conductivity and/or lower Km-values for creatine. They are much better
 CC suited to detection methods for creatine. The present sequence encodes a
 CC mutant Erwinia creatinase from the present invention

XX Sequence 1212 BP; 239 A; 393 C; 359 G; 221 T; 0 U; 0 Other;

Query Match

Best Local Similarity 80.6%; Score 976.8; DB 8; Length 1212;

Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

1 ATGACTGACGACATGTTGCACTGATGAATGSCACACGCGAGAAATTTTCGCGC 60

1 ATGACTGACGACATGTTGCACTGATGAATGSCACACGCGAGAAATTTTCGCGC 60

61 TTTTGGATGCGGAGATGACCGCGCGCAAAAGCATGTGCGGCGTGTGCGCAAGAC 120

61 TTTTGGATGCGGAGATGACCGCGCGCAAAAGCATGTGCGGCGTGTGCGCAAGAC 120

121 AATGTGATGCGCGCGTGTGCACTCTTATCACTGATCACTAATTCGCGTGTG 180

121 AATGTGATGCGCGCGTGTGCACTCTTATCACTGATCACTAATTCGCGTGTG 180

122 GACGTGAGCGTGTGCGTGTGCACTCTTATCACTGATCACTAATTCGCGTGTG 180

122 GACGTGAGCGTGTGCGTGTGCACTCTTATCACTGATCACTAATTCGCGTGTG 180

181 TACTGTATTTTGGACGCAATGACGATGTCATGACCAACAACCCACAGCATTC 240

181 TACTGTATTTTGGACGCAATGACGATGTCATGACCAACAACCCACAGCATTC 240

181 TACTGTATTTTGGACGCAATGACGATGTCATGACCAACAACCCACAGCATTC 240

241 TGGGCGGCGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

241 TGGGCGGCGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

241 TGGGCGGCGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

301 ACCGACTGCG 360

301 ACCGACTGCG 360

301 ACCGACTGCG 360

361 GCGATGCGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTG 420

361 GCGATGCGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTG 420

361 GCGATGCGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTG 420

421 CTACCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 480

421 CTACCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 480

421 CTACCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 480

481 TCGCTGCAAGACGAGAGTGTGTCGCGAGGCGCGCGCGCGCGCGCGCGCGCG 540

481 TCGCTGCAAGACGAGAGTGTGTCGCGAGGCGCGCGCGCGCGCGCGCGCGCG 540

481 TCGCTGCAAGACGAGAGTGTGTCGCGAGGCGCGCGCGCGCGCGCGCGCGCG 540

481 TCGCTGCAAGACGAGAGTGTGTCGCGAGGCGCGCGCGCGCGCGCGCGCGCG 540

541 GCGTGGCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 600

541 GCGTGGCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 600

541 GCGTGGCGGCGGCGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACT 600

601 AATGCGAGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTGATCACT 660

601 AATGCGAGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTGATCACT 660

601 AATGCGAGATGAGTTGCACTGATCACTGATCACTGATCACTGATCACTGATCACT 660

661 ACCTGTTTCAGTGTGCGGCGATCAACACGCGCGCGCGCGCGCGCGCGCGCGCG 720

661 ACCTGTTTCAGTGTGCGGCGATCAACACGCGCGCGCGCGCGCGCGCGCGCGCG 720

661 ACCTGTTTCAGTGTGCGGCGATCAACACGCGCGCGCGCGCGCGCGCGCGCGCG 720

661 ACCTGTTTCAGTGTGCGGCGATCAACACGCGCGCGCGCGCGCGCGCGCGCGCG 720

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781 GCGCTGAGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 840

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841 AAGAACGTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 900

901 GACATGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 960

901 GACATGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 960

901 GACATGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 960

961 TTCGCTGAGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1020

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961 TTCGCTGAGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1020

1021 GACCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1080

1021 GACCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1080

1021 GACCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1080

1081 ATGCTGATGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1140

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1141 ATCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1200

1141 ATCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1200

1141 ATCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1200

1141 ATCTGCGGCGGATGATCTTTCGCTCAACCTTCCGATGATCTGCGTACTACAC 1200

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FT      /product= "creatinase mutant CT62"
FT      /note= "no stop codon given"
XX      BP1298213-A1.
XX
XX      02-APR-2003.
XX
XX      17-SEP-2002; 2002EP-00020793.
XX
XX      20-SEP-2001; 2001EP-00121780.
XX
XX      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX      Shao Z, Schmuck R, Kratzsch P, Kenkies J, Weisser H;
XX      WPI: 2003-383834/37.
XX      P-PSDB; ABR43479.
XX
XX      New variant of an Erwinia-type creatinase modified relative to a wild-
XX      type creatinase having creatinase activity, useful for determining
XX      creatinase and/or creatine concentration in a sample.
XX
XX      Example 4; Page 37-39; 51pp; English.
XX
XX      The present invention describes a variant of an Erwinia-type creatinase
XX      (I) modified relative to a wild-type creatinase having creatinase
XX      activity. The variant comprises at least one amino acid substitution at a
XX      position of the fully defined 404 amino acid sequence given in ABR43467.
XX      These are selected from N130, N203, I278, I1304 and P355. Creatinase has
XX      the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.
XX      Also described is a reagent (II) for determining creatine concentration
XX      Erwinia-type creatinase variant. The variant is useful for determining
XX      creatinase and/or creatine concentration in a sample. Measuring
XX      creatinase and creatine are useful for diagnosing uremia, chronic
XX      nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some
XX      other related diseases. The mutant enzymes have improved stability, lower
XX      conductivity and/or lower Km-values for creatine; they are much better
XX      suited to detection methods for creatine. The present sequence encodes a
XX      mutant Erwinia creatinase from the present invention
XX
XX      Sequence 1212 BP; 239 A; 393 C; 360 G; 220 T; 0 U; 0 Other:
XX
XX      Query Match      80.3%; Score 973.6; DB 8; Length 1212;
XX      Best Local Similarity 87.7%; Pred. No. 1.5e-155;
XX      Matches 1063; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY      361 CGCATCGGATGAGTTGACCACTGCAATCTTCGACTTCCGCCCGCAGCTCGAGAGGCC 420
DB      361 CGCATCGGATGAGTTGACCACTGCAATCTTCGACTTCCGCCCGCAGCTCGAGAGGCC 420
QY      421 CTACCGGGGCGTGCATCTGTCGACATCAGCCCTCGATGATGATGCGCAACATCAAG 480
DB      421 CTACCGGGGCGTGCATCTGTCGACATCAGCCCTCGATGATGATGCGCAACATCAAG 480
QY      481 TCGCTCGAAGAGCAGAGTGTATCCGCGAGGCGCCGCGTGTGACCTCGCGCGCG 540
DB      481 TCGCTCGAAGAGCAGAGTGTATCCGCGAGGCGCCGCGTGTGACCTCGCGCGCG 540
QY      541 GCGTGGCGGCTGCGCATCAAGGCGCGTGTGCGCGAGCATGAAGTGCATCGCCACACC 600
DB      541 GCGTGGCGGCTGCGCATCAAGGCGCGTGTGCGCGAGCATGAAGTGCATCGCCACACC 600
QY      601 AATGCGATGATCGCGAGATCGCAAAATGCTTCCCTTGTGAGGTGATGACACCTGG 660
DB      601 AATGCGATGATCGCGAGATCGCAAAATGCTTCCCTTGTGAGGTGATGACACCTGG 660
QY      661 ACCTGGTTCAGTGGGATCAACACCGAGCGGCAACATCCGATCAACACCGCATC 720
DB      661 ACCTGGTTCAGTGGGATCAACACCGAGCGGCAACATCCGATCAACACCGCATC 720
QY      721 GTGCAATCGGCGGATCTTCTGCTCAACACTTCCGATGATCTTGGGCTACTACAC 780
DB      721 GTGCAATCGGCGGATCTTCTGCTCAACACTTCCGATGATCTTGGGCTACTACAC 780
QY      781 GCGCTGAGCGGACGCTGTTGCGACCATGTCATGACGCGAGCTCGACATCTGGAG 840
DB      781 GCGCTGAGCGGACGCTGTTGCGACCATGTCATGACGCGAGCTCGACATCTGGAG 840
QY      841 AAGAACTGCGCGTGCATCGCGCGGCTGCGAGTCAACCGCGCGCGCTGCAAG 900
DB      841 AAGAACTGCGCGTGCATCGCGCGGCTGCGAGTCAACCGCGCGCGCTGCAAG 900
QY      901 GATATCGGATCGGATCTGACGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB      901 GATATCGGATCGGATCTGACGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY      961 TTGCGCTAGCGGATCTTCTGCGGCTGCTTCCACTACATGAGCGCGGCGCG 1020
DB      961 TTGCGCTAGCGGATCTTCTGCGGCTGCTTCCACTACATGAGCGCGGCGCG 1020
QY      1021 GAGCTGCGGAGATCGACATCGACATCGAGCTGAAGCCGCGATGCTTCTCAATGAGCGG 1080
DB      1021 GAGCTGCGGAGATCGACATCGACATCGAGCTGAAGCCGCGATGCTTCTCAATGAGCGG 1080
QY      1081 ATGCTGATGCTGCGGAGGCGATGCGCGGCTGCGCGGCTGCTGCGGAGCAGACATCTCTG 1140
DB      1081 ATGCTGATGCTGCGGAGGCGATGCGCGGCTGCGCGGCTGCTGCGGAGCAGACATCTCTG 1140
QY      1141 ATCGTGGGAGGAGAGCGTGCAGAGACATCAACCGGCTTCCGTTGCTGCGGAGCAGACC 1200
DB      1141 ATCGTGGGAGGAGAGCGTGCAGAGACATCAACCGGCTTCCGTTGCTGCGGAGCAGACC 1200
QY      1201 ATCATCGGCAAC 1212
DB      1201 ATCATCGGCAAC 1212

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Search completed: November 19, 2004, 16:39:06
Job time : 664 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2004, 12:40:44 ; Search time 124 Seconds
(without alignments)
6947.388 Million cell updates/sec

Title: US-10-807-228-2

Perfect score: 1212
Sequence: 1 ATGACTGACGACATCTTGCA.....AACACACATCATCCGCAAC 1212

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1210.4	99.9	1212	3	US-08-799-897-2
2	1204	99.3	1215	2	US-08-947-726A-1
3	74	6.1	858	4	US-09-252-991A-4171
4	74	6.1	963	4	US-09-252-991A-4435
5	74	6.1	1176	4	US-09-252-991A-4314
6	64.8	5.3	3157	2	US-08-939-002A-1
7	63.6	5.2	2064	1	US-08-343-428-1
8	62.4	5.1	1294	3	US-09-025-691-2
9	60.6	5.0	1599	4	US-09-475-515-54
10	60.6	5.0	2112	4	US-09-475-515-57
11	60.6	5.0	2112	4	US-09-475-515-56
12	60.6	5.0	2181	4	US-09-475-515-58
13	60.6	5.0	2634	4	US-09-475-515-64
14	60.6	5.0	4766	4	US-09-475-515-73
15	59.6	4.9	2712	3	US-09-025-691-4
16	59.2	4.9	1056	4	US-09-266-965-66
17	59.2	4.9	53500	4	US-09-266-965-76
18	58.4	4.8	1965	4	US-09-220-132-21
19	57.6	4.8	1293	2	US-08-924-440-1
20	56.8	4.7	2943	1	US-08-042-747A-7
21	56.4	4.7	1005	4	US-09-252-991A-1549
22	56.4	4.7	1590	4	US-09-252-991A-1617
23	56.4	4.7	1693	3	US-09-320-878-23
24	56.2	4.6	1693	3	US-09-141-908-19
25	56.2	4.6	1693	4	US-09-657-440-23
26	55.8	4.6	1399	1	US-08-471-033-24
27	55.8	4.6	1399	1	US-08-471-033-24

28	55.8	4.6	1399	2	US-08-471-044-24	Sequence 24, Appl
29	55.8	4.6	1399	2	US-08-463-483A-24	Sequence 24, Appl
30	55.8	4.6	1399	2	US-08-471-046A-24	Sequence 24, Appl
31	55.8	4.6	1399	2	US-08-470-566B-24	Sequence 24, Appl
32	55.8	4.6	1399	2	US-08-469-334-24	Sequence 24, Appl
33	55.8	4.6	1399	3	US-09-300-529-24	Sequence 24, Appl
34	55.6	4.6	1082	4	US-09-881-165-4	Sequence 4, Appl
35	55.4	4.6	2655	1	US-08-471-033-17	Sequence 17, Appl
36	55.4	4.6	2655	1	US-08-471-033-26	Sequence 26, Appl
37	55.4	4.6	2655	2	US-08-471-044-17	Sequence 17, Appl
38	55.4	4.6	2655	2	US-08-471-044-26	Sequence 26, Appl
39	55.4	4.6	2655	2	US-08-463-483A-17	Sequence 17, Appl
40	55.4	4.6	2655	2	US-08-463-483A-26	Sequence 26, Appl
41	55.4	4.6	2655	2	US-08-471-046A-17	Sequence 17, Appl
42	55.4	4.6	2655	2	US-08-471-046A-26	Sequence 26, Appl
43	55.4	4.6	2655	2	US-08-470-566B-17	Sequence 17, Appl
44	55.4	4.6	2655	2	US-08-470-566B-26	Sequence 26, Appl
45	55.4	4.6	2655	2	US-08-469-334-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-799-897-2
Sequence 2, Application US/08799897
Patent No. 6080553
GENERAL INFORMATION:
APPLICANT: Sogabe, Atsushi
APPLICANT: Hattori, Takashi
APPLICANT: Nishiyama, Yoshiaki
APPLICANT: Kawamura, Yoshihisa
TITLE OF INVENTION: NOVEL CREATINE AMIDINOHYDROLASE, PRODUCTION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799, 897
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 25435/1996
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Robert F. Green
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 78064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1212 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORGANISM: Alcaligenes faecalis
STRAIN: TE3581 (ERM P-14237)
FEATURE:

NAME/KEY: CDS
LOCATION: 1 to 1212
us-08-799-897-2

Query Match 99.9%; Score 1210.4; DB 3; Length 1212;
Best Local Similarity 99.9%; Pred. No. 5.1e-255;
Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACGACGACATGTTGACGATGAAATGGCAACAAGGCGAAGAAATTTTCCCG 60
DB 1 ATGACGACGACATGTTGACGATGAAATGGCAACAAGGCGAAGAAATTTTCCCG 60
QY 61 TTTTCGATGCGGATGACCGCGCCGCAAAAGCATTCGCGGCGATGGCGAAGAC 120
DB 61 TTTTCGATGCGGATGACCGCGCCGCAAAAGCATTCGCGGCGATGGCGAAGAC 120
QY 121 AATGTCGATGCGGCGCTGTTCACTTTATCACTGATCACTACTATTCCGGCTGGCTG 180
DB 121 AATGTCGATGCGGCGCTGTTCACTTTATCACTGATCACTACTATTCCGGCTGGCTG 180
QY 181 TACTGCTATTTGGAGAGCAAGTACGGCATGTCATGACCAACAACCGCACAGAT 240
DB 181 TACTGCTATTTGGAGAGCAAGTACGGCATGTCATGACCAACAACCGCACAGAT 240
QY 241 TCGGCGGCGCATGACGCGCGCGCAGCCCTGCGCGCGCAGCTTGGCGCAACAATCACTAC 300
DB 241 TCGGCGGCGCATGACGCGCGCGCAGCCCTGCGCGCGCAGCTTGGCGCAACAATCACTAC 300
QY 301 ACCGACTGGCGCGCGCAATTTCTATTCGCGCGCTGCGCACGTCGACGCGCGCAAG 360
DB 301 ACCGACTGGCGCGCGCAATTTCTATTCGCGCGCTGCGCACGTCGACGCGCGCAAG 360
QY 361 CGCATTCGGATGAGTTGCAACAAGTCTGACATTCGCGCGCGCAGCTTGGCGCAAGCC 420
DB 361 CGCATTCGGATGAGTTGCAACAAGTCTGACATTCGCGCGCGCAGCTTGGCGCAAGCC 420
QY 421 CTACCGGCGCGCATGCTTCTGACATCAACCGCCCTGATGATGATGCGACATCAAG 480
DB 421 CTACCGGCGCGCATGCTTCTGACATCAACCGCCCTGATGATGATGCGACATCAAG 480
QY 481 TCGCTCGAAGAGCAGAACTGATTCGCGAAGCGCGCGCGTGTGACGTCGCGCGCGCG 540
DB 481 TCGCTCGAAGAGCAGAACTGATTCGCGAAGCGCGCGCGTGTGACGTCGCGCGCGCG 540
QY 541 GCGTCGCGGCGCTGCGCATCAAGGCGCGCGCGCGCGCATGAAGTGGCGATCCGCAACC 600
DB 541 GCGTCGCGGCGCTGCGCATCAAGGCGCGCGCGCGCGCATGAAGTGGCGATCCGCAACC 600
QY 601 AATGCGATGATCGCGAGATGCGCAATGCTTCCCTTGTGAGAGTGAAGTGAACCTGG 660
DB 601 AATGCGATGATCGCGAGATGCGCAATGCTTCCCTTGTGAGAGTGAAGTGAACCTGG 660
QY 661 ACCTGTTTCAGTTCGCGGATCAACCGGCGCGGCAATCCGCTACCAACCGCATC 720
DB 661 ACCTGTTTCAGTTCGCGGATCAACCGGCGCGGCAATCCGCTACCAACCGCATC 720
QY 721 GTGCAATCGCGGACATCTTTCGCTCAACCTTCCGATATCTTGGGCTACTACAC 780
DB 721 GTGCAATCGCGGACATCTTTCGCTCAACCTTCCGATATCTTGGGCTACTACAC 780
QY 781 GCGCTGAGAGCGACGCTGTTGCGACCAATGTCGATGACGCGAGCTGACATCTGGAG 840
DB 781 GCGCTGAGAGCGACGCTGTTGCGACCAATGTCGATGACGCGAGCTGACATCTGGAG 840
QY 841 AAGAAAGTGGCGGTCATTCGCGCGGCTGCGATCAACCGCGCGCGCGCTGCAAG 900
DB 841 AAGAAAGTGGCGGTCATTCGCGCGGCTGCGATCAACCGCGCGCGCGCTGCAAG 900
QY 901 GACATCGCGATGAGTCAACAAGATGACCGGAGTGGGACCTGCTGAAGTACCGCTCC 960
DB 901 GACATCGCGATGAGTCAACAAGATGACCGGAGTGGGACCTGCTGAAGTACCGCTCC 960
QY 961 TTGGGCTATGGCACTCTTGGGCGCTGCTGCACTACTAGTGGGAGCGCGCTG 1020

DB 961 TTGGGCTATGGCACTCTTGGGCGCTGCTGCACTACTAGTGGGAGCGCGCTG 1020
QY 1021 GAGTTCGCGAGACATGACACCGAGCTGAAGCCCGCATGCTGCTCAATGAGCGG 1080
DB 1021 GAGTTCGCGAGACATGACACCGAGCTGAAGCCCGCATGCTGCTCAATGAGCGG 1080
QY 1081 ATGTCGATGCTGCGGAGGCGCATGCGCGGCTGCGGCGCTATCGGAGACATCTCTG 1140
DB 1081 ATGTCGATGCTGCGGAGGCGCATGCGCGGCTGCGGCGCTATCGGAGACATCTCTG 1140
QY 1141 ATGTCGCGGAGAGACGCTGCGGAGACATCAACCGCTTCCGCTGCGGAGCAAC 1200
DB 1141 ATGTCGCGGAGAGACGCTGCGGAGACATCAACCGCTTCCGCTGCGGAGCAAC 1200
QY 1201 ATCATCGCGCAAC 1212
DB 1201 ATCATCGCGCAAC 1212

RESULT 2
US-08-947-726A-1
Sequence 1, Application US/08947726A
Patent No. 5932466
GENERAL INFORMATION:
APPLICANT: Furukawa, Keisuke
APPLICANT: Ichikawa, Toshio
APPLICANT: Suzuki, Masaru
APPLICANT: Koyama, Yasuji
TITLE OF INVENTION: A NOVEL CREATINE AMIDINOHYDROLASE GENE,
TITLE OF INVENTION: A NOVEL RECOMBINANT DNA, AND A PROCESS FOR PRODUCING
NUMBER OF INVENTIONS: 5
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,726A
FILING DATE: 09-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,444
FILING DATE: 27-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 94/235737
FILING DATE: 29-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence III, Stanton T.
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-120-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Alcaligenes sp. KS-85
STRAIN: FERM BP-4487

Db 501 GCACCTGGGGGATATCG---GCCAATCATCCAGAGACCGGAAAAAGACGGCTTCTC 557
Qy 951 GTACCGCTCTTCCGCTGATGAGCCATCTCTTCCGCGTGTCTGCACTACTACGATCGCGA 1010
Db 558 GGTGTCTCCGGAATACGCGGCGCATGCGCATCGGCAAGGTGTCTC---ACGAGAGCGCGCA 614
Qy 1011 GCGCGCGGTGGACTCGCGAGACATCGACACCGAGCTGAAGCCCGGCACTGTGTCTC 1070
Db 615 GGTCTCTCACTACGCTGTGTGCGGATACCGGCGATCGAGTGAAGAGGCAATGATCTTCAC 674
Qy 1071 CATGAGCCGATGATGATGCTGCGGAGGCGATCGCGGCTGCGGCGCTATCGGAGCA 1130
Db 675 CATCGAGCCGATATCAACAGGCGCGCGCGAGAGCCCGCTGTGCGGACGCTGTGAC 754
Qy 1131 CGACATCTGTATGTGTGGGAG 1152
Db 735 CGCGATCACCAGAGACCGCAAG 756

RESULT 4
US-09-252-991A-4435/c
; Sequence 4435, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4435
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4435

Query Match 6.1%; Score 74; DB 4; Length 963;
Best Local Similarity 46.3%; Pred. No. 2.5e-07;
Matches 316; Conservative 0; Mismatches 360; Indels 6; Gaps 2;
Qy 471 CACCATCAAGTCTCGAAGAGCAAGATGATCCGCAAGCGCCGCGTGTGACGT 530
Db 922 CACCATCAAGAGCGCCGAGATATCGAAGAGATGCGCATCGCGCGCTGGCGCGCA 863
Qy 531 CCGCGCGCGGCTGCGCGGCTGCGCATCAAGCGCGGCTGCGCGAGCATGAGTGGCAT 590
Db 862 AGTGTGGAATGATGCGGAGACATCAAGCGCGGCTGCAACCGAGAGTGTGATCG 803
Qy 591 CGGCACCAACATGAGATGATCGCGAGATCGCAATGCTTCCCTGTGTGAGTGTAT 650
Db 802 CATCTGCCACGATTAATGTCAACAGAGCAAGAGGAGATTCCTGCCCCCTGAATCAAA 743
Qy 651 GGACACCTGAGCTGTTCAGTGTGCGGATCAACACCGAGCGCGGCAACATCCGTCAC 710
Db 742 GGGCTTTCCCAAGTATGATCGACCTGTGATCAACATGTGTGTGCTGCAATGCGCAAA 683
Qy 711 CAACCGCATGTGCAATCGCGGAGCATCTTTGCTCAACACTTCCGATGATCTTGG 770
Db 682 CGAAGAGCGCTGAAGAGAGCGACATCTCTCAACGTGCAATCAACCGTATCAAGAGCG 623
Qy 771 CTACTACACCGCGCTGAGAGCGACGCTGTCTGCGACCAATGTGATGAGCGAGCTCGA 830
Db 622 CTACCAACCGCGAGACCAAGATGTTCTGTGTGCGCAAGATCCCGCAATGGCGGACCG 563
Qy 831 CATCTGGAGAGAAAGTGTGCGCTGTGATCGCGCGGCTGAGCTGATCAAGCGGCGCG 890
Db 562 CTTCTGCGAGATCAACCAAGAAATGATGTAACAAGGCGATTTCCGTGTGCGTCCGCGCGC 503

Qy 891 GCGCTGCAAGACATTCGCGATGAGCTCAACGATGTACCGGAGTGGAGCTGCTGAA 950
Db 502 GCACCTGGGCGATATCG---GCCAATCATCCAGAGACCGGAAAAAGACGGCTTCTC 446
Qy 951 GTACCGCTCTTCCGCTATGAGCCATCTCTTCCGCGTGTCTGCACTACTACGATCGCGA 1010
Db 445 GGTGTCTCCGGAATACGCGGCGCATGCGCATCGGCAAGGTGTCTC---ACGAGAGCGCGCA 389
Qy 1011 GCGCGCGGTGGACTCGCGAGACATCGACACCGAGCTGAAGCCCGGCACTGTGTCTC 1070
Db 388 GGTCTCTCACTACGCTGTGTGCGGATACCGGCGATCGAGTGAAGAGGCAATGATCTTCAC 329
Qy 1071 CATGAGCCGATGATGATGCTGCGGAGGCGATCGCGGCTGCGGCGCTATCGGAGCA 1130
Db 328 CATCGAGCCGATGATCAACAGGCGCGCGCGAGAGCCCGCTGTGCGGACGCTGTGAC 269
Qy 1131 CGACATCTGTATGTGTGGGAG 1152
Db 268 CGCGATCACCAGAGACCGCAAG 247

RESULT 5
US-09-252-991A-4314
; Sequence 4314, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4314
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4314

Query Match 6.1%; Score 74; DB 4; Length 1176;
Best Local Similarity 46.3%; Pred. No. 2.6e-07;
Matches 316; Conservative 0; Mismatches 360; Indels 6; Gaps 2;
Qy 471 CACCATCAAGTCTCGAAGAGCAAGATGATCCGCAAGCGCCGCGTGTGACGT 530
Db 244 CACCATCAAGAGCGCCGAGATATCGAAGAGATGCGCATCGCGCGCTGGCGCGCA 303
Qy 531 CCGCGCGCGGCTGCGCGGCTGCGCATCAAGCGCGGCTGCGCGAGCATGAGTGGCAT 590
Db 304 AGTGTGGAATGATGCGGAGACATCAAGCGCGGCTGCAACCGAGAGTGTGATCG 363
Qy 591 CGGCACCAACATGAGATGATCGCGAGATCGCAATGCTTCCCTGTGTGAGTGTAT 650
Db 364 CATCTGCCACGATTAATGTCAACAGAGCAAGAGCGATTCCTGCCCCCTGAATCAAA 423
Qy 651 GGACACCTGAGCTGTTCAGTGTGCGGATCAACACCGAGCGCGGCAACATCCGTCAC 710
Db 424 GGGCTTTCCCAAGTATGATCGACCTGTGATCAACATGTGTGTGCTGCAATGCGCAAA 483
Qy 711 CAACCGCATGTGCAATCGCGGAGCATCTTTGCTCAACACTTCCGATGATCTTGG 770
Db 484 CGAAGAGCGCTGAAGAGAGGAGCATCTCAAGTCAACATCAACCGTATCAAGAGCG 543
Qy 771 CTACTACACCGCGCTGAGAGCGACGCTGTCTGCGACCAATGTGATGAGCGAGCTCGA 830
Db 544 CTACCAACCGCGAGACCAAGATGTTCTGTGTGCGCAAGATCCCGCAATGGCGGACCG 603
Qy 831 CATCTGGAGAGAAAGTGTGCGCTGTGATCGCGCGGCTGAGCTGATCAAGCGGCGCG 890

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Db      604 CCTCTGCAGATCACCAGAAATGTCATCAAGGGATTTCCGTGTGCTCCGGCCG 663
Qy      891 GCGCTGCAAGACATGCCATTCGACTCAACGAGATGTACCGAGTGGAGCTGCTGAA 950
Db      664 GCACCTGGGGGATATCG--GCCAATTCATCCAGAAAGCACCGGAAAGACGGCTTCTC 720
Qy      951 GTACCGCTCTTGGGCTATGAGCCATCCTTCGGCGTGTGTGCTGACCTACAGCGTCCGA 1010
Db      721 GGTGTCTCCGAATATCTGCGGCCATGCGCATGCGCAAGGTTC--ACGAGAGCCGCA 777
Qy      1011 GCGCGCGTGTGAGCTGCGCGAGACATTCGACACCGAGCTGAGCCCGCATGTGTGCTC 1070
Db      778 GGTCTTCCTCACTAGGTGTGTGCGGGTACCGGCATCGAGCTGAGAGGACATGATCTTCAC 837
Qy      1071 CATGAGCCGATGTGTGTCTGCGGAGGGCATGCGCGGTGCGCGGCTATTCGACGA 1130
Db      838 CATCGAGCGATATCAACGAGGCGCGCCGAGAGCCGCTGCGCGACGCGTGGAC 897
Qy      1131 CGACATCTGATGTGTGGGAG 1152
Db      898 CGGATCACCAGACCGCAG 919

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RESULT 6

US-08-939-002A-1
Sequence 1, Application US/08939002A
Patent No. 5849529

GENERAL INFORMATION:
APPLICANT: HAYASHI, KIYOSHI
APPLICANT: LIU, AIMIN
APPLICANT: LI, HEBIAO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: KITAHARA, YOSHIKI
TITLE OF INVENTION: CELLOBIOSE PHOSPHORYLASE GENE, VECTOR
NUMBER OF SEQUENCES: 16
TITLE OF SEQUENCES: AND TRANSFORMANT CONTAINING SAID GENE
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,002A
FILING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 221193/1997
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4361-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Cellvibrrio gilvus

STRAIN: ATCC 13127
INDIVIDUAL ISOLATE: Direct Origin: puc-2
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 359..2824
OTHER INFORMATION: /note="METHOD FOR DETERMINING
OTHER INFORMATION: SEQUENCE: E"
FEATURE:
NAME/KEY: CDS
LOCATION: 359..2824
US-08-939-002A-1

Query Match 5.3%; Score 64.8; DB 2; Length 3157;
Best Local Similarity 42.1%; Pred. No. 3.3e-05;
Matches 436; Conservative 0; Mismatches 597; Indels 3; Gaps 1;

```

Qy      180 GTACTGTATTTTCGACGCAAGTACGGCATGTGTCAATCGACCAACAGCCGACGAT 239
Db      802 GTTCGTGAGTTCGTGCTGTGAGACGGCGACAGACCAAGACGATACAGCGCAACT 861
Qy      240 TTCGGCCGGCATGACGCGGCGCAAGCCCTGCGCCGACCTTCGGGACATCACTTA 299
Db      862 GTCGATCGGCGAGTTCAGGTGAGAGCAGACGCGCGACCGGCTGCGCATTCACAA 921
Qy      300 CACGACATGCGCGCGGACCAATTTCTATCGCGCGGCGGCGGACGCTGACCGAGCGCCAA 359
Db      922 GACCGAGTACCGCGAGCGCGCGGACCACTACCGCTGTTTGGCGTGAACACCGCGCGA 981
Qy      360 GCGCATCGGCGATGAGTTTCGACCAAGTCATTCGATTCGACCGCGCATGCGAGAAC 419
Db      982 CGGCTTCGACGACGACCGGACACGTTGTTGGCGGATCACTGCTGGGCGAGGCGTC 1041
Qy      420 CTTACCGGGCGTTCGACTTCGTGATCATGACGACGCTTCGTGATGTGATTCGACATCAA 479
Db      1042 CTTCCCGCGCGCGGAGATCGCGGATCGGTTCGCTGCTGCTGATCCGATTCGCTC 1101
Qy      480 GTGCTCGAAGAGAGAGAGTGTATCGCGAAGCGCGCGGCTGTGAGCTGCGCGCGC 539
Db      1102 GCACTTCCTGCGCGGAGTGTGAGCTGACGCGCGGAGTTCGCGACCTGCTTACGTGTGG 1161
Qy      540 GGCCTGCGCGGCTGCTCATGAGCGCGGCGGCGGAGCATGAGTGGCGATGCGCACAC 599
Db      1162 CTACCTGAGAGAACCCGACGAGAGAGAGTGGCGGACGACGCGCACAGTGTGACAA 1221
Qy      600 CAATGCGATATCCCGGAGATGCCAAATCTTTCCCTTCGTGAGCTGATGACACTG 659
Db      1222 GCGCGCGCGGACGCGCTGCTGGCGGCTGCGGCTGCGAGCGAGTTCGACGCGCCCT 1281
Qy      660 GACCTGTTCGATCGGCGCATCAACGAGCGCGGCGGACATTCGGGTCAACACCGCAT 719
Db      1282 GAGGCGCTGAACCTCTTACGAGAACCTGCTTTCGAGATCTGGTGTCAACACCGA 1341
Qy      720 CTTGCAATCCGCGGACATCTTTTCGCTCAACACTTTCGAGATCTTTCGCTACTAC 779
Db      1342 CGAGAGCTCGACGAGATGTGAACATCTGAAACAGTACAGAGTGTGATGATGATGAT 1401
Qy      780 GCGCTGAGAGCGACGCTGTTTGTGACCATGTGATGACGCGGACCTGACATCTGGGA 839
Db      1402 CATGTGCGGCTCGGCGGTGTTCTTTCGAGACGCGGCAATCGCGCGGAGTGGCTTCGCGCA 1461
Qy      840 GAAAGACGTGGCGGTGATTCGCGCGGCTGAGTGTGATGAGC---CGGCGCGCGCTG 896
Db      1462 CTCGACACGAGACTCTCTGGGCTTGTGTGACCTGATTCGCGAGCGCGCGGAGCGAT 1521
Qy      897 CAAGGACATCGGCATCGACTCAACGAGATGTACCGGAGTGGACCTGCTGAAGTACCG 956
Db      1522 CATGACATCGGCTGAGAGGATGTTGCGGAGCGGCTCGGATTCACACGATACGACGCT 1581
Qy      957 CTCCTTGGCTATGCGCACTCTTGTGGGCTGTGTCGACATCTACGATGATGAGGCGCG 1016
Db      1582 CACGAGCGCGGAGCAACGACATCGGCTTTCGAGCGACGCGCTGTGCTCAT 1641
Qy      1017 COTGAGCTGCGCGGAGCATGACACGAGCTGAAGCCGCGCATGTGTCTCATGGA 1076

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Db 1642 CGCGGGGCTGCGCGCGATCAAGAGTCCGGGACTGGGGATCTCGACGAGCCGT 1701
Qy 1077 GCGGATGATATCTGCGGAGGCGATGCCGGTCCGGGCGCTATGCGAGACGACAT 1136
Db 1702 GCGGTTGACAGAGAGCCCGCTCCGAGGTCCCGCTGTTGACACCTGACGGGCTCTT 1761
Qy 1137 CCTGATGTCGGGAGAGCGTCCGAGACATCACCGGCTTCCGTTGCGTCCGAGACA 1196
Db 1762 CCAAGTTACGGTTCAGAACCGCGCCCGACGCGCTGCGCTCATGCGCGCTCCACTG 1821
Qy 1197 CACCATATTCGCAAC 1212
Db 1822 GAACGACTGCTCAAC 1837

RESULT 7
US-08-343-428-1
; Sequence 1, Application US/08343428
; Patent No. 5665586
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Etano
; APPLICANT: Tezuka, Hirohige
; APPLICANT: Kitadokoro, Kengo
; APPLICANT: Shin, Naosaru
; APPLICANT: Teraoka, Hiroshi
; TITLE OF INVENTION: No. 5665586el Protease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720KB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS Dos 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,428
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; Prior APPLICATION DATA:
; APPLICATION NUMBER: PCT/793/00592
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: JAPAN 4-126511
; FILING DATE: 19-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27794
; REFERENCE/DOCKET NUMBER: SHN-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Streptomyces fradiae
; FEATURE:
; NAME/KEY: -35 signal
; LOCATION: 359..364
; IDENTIFICATION METHOD: by experiment
; NAME/KEY: -10 signal
; LOCATION: 378..383
; IDENTIFICATION METHOD: by experiment
; NAME/KEY: CDS

; LOCATION: 435..1505
; IDENTIFICATION METHOD: by experiment
; NAME/KEY: sig peptide
; LOCATION: 435..944
; IDENTIFICATION METHOD: by experiment
US-08-343-428-1

Query Match 5.2%; Score 63.6; DB 1; Length 2064;
Best Local Similarity 44.5%; Pred. No. 5.5e-05;
Matches 343; Conservative 0; Mismatches 419; Indels 8; Gaps 2;

Qy 103 GGCTGATGCGCCAGAACATGTCATGCGGCGCTGTTACCTTTATCATGATCAAC 162
Db 992 GCCTTCAAGCTACCAAGAGCGGTTGGTACTTCTGACCGCGGACATGACCAAC 1052
Qy 163 TACTATTCGGGCTGGCTGCTACTGCTATTTCGAGCGAGATAGGATGATCGACAC 222
Db 1053 CTCTGCTCCACTGTGTCTCCACC--TCCGCGGACAGTTCATCGGCTTCGCGAGGC 1109
Qy 223 AACAGCGCAGCAGATTTCCGCGGATTCGAGCGGCGGCGAGCCCTGGCGCGAGCTTC 282
Db 1110 ACCAGCTTCCGACCAAGACATGAGCATGTCGCTTACAGACACCAACAGTGCAG 1169
Qy 283 GCGCACAATCACCCTAGACCGACTGGCGCGCGCAATTTCTATCGCGCTGGCGCAG 342
Db 1170 GCGCGGGTCACTGTGACAGGGGGGCTACAGACATCGCCTCGCGGCGGACGCGCTC 1229
Qy 343 CTGACCAAGGGGCGCAAGCGCATGCGCATGAGTTGACACAGTCAATTCGACTTCGC 402
Db 1230 GTGGGCGCAGGCGCATAGAGGCGCTCCAGACCAAGTCCAGCGGCGACCGTCAAC 1289
Qy 403 CGCCAGCTCGAGAGAGCCCTACCGGGCGTCCGATGTCGATCAGCGCGCGCTGATG 462
Db 1290 GCGCTCAAGTCACTGATCACTACAGACAGCGCCCGTTCAGGATGTTCCGACAGCC 1349
Qy 463 TGGATGCGCACCATCAAGTCTCGAAGAGAGAACTGATCCGGAAGCGCGCGCTG 522
Db 1350 GCGTCTCGCGCGCGGAGACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1409
Qy 523 TGTGACGTGCGGCGCGCGCGCTGCGCGCGCTGCGATCAAGCGCGGTGCCGAGCATGA 582
Db 1410 ATCCACTCGGGGAGCTCCGCGGCGACCGGCGCAACCGCTCGCATCCACGCGCGT 1469
Qy 583 GTGGGATGCGCACCACCAATGCGATGATCGCGGATCGCAATTCGTTCCCTTCG 642
Db 1470 GCGGAGCGCTGAGGCTTATGCGGTGAAC-----GTGACTGACCCCGCGCGCGC 1524
Qy 643 GAGCTGATGACACCTGAGCTGTTCCAGTCCGAGCATCAACCGAGCGCGCGCAAT 702
Db 1525 GGGCGGAGTGGCAGAGTGGGGGTATGATGTGTCATACCGCGCAACCTACAGAG 1584
Qy 703 CCGGTACCAACCGCATGTGCAATCGCGCGCATCTTTGGCTCAACACTTCCGATG 762
Db 1585 CTGGCACCAGCGCGTGTCTGATTCGCGCGCTTCCTCCAGAGAGCGCTTCAGAGCGAGC 1644
Qy 763 ATCTTGGCTACTACAGCGCGTGGAGGCAAGCTGTTCTGAGACCATGTCATGAGCGC 822
Db 1645 CTGAGCGAGAGAGATGGAGACGCGCTCGCGCGCTTCACAGCGCTACCGAGAGCGC 1704
Qy 823 AGCTTCGACTGTGGAGAGAACGTGCGCTGATCCGCGCGGCGCTGCA 872
Db 1705 GCGCGGCGGATGTGGCGCACGAGCGTCTGATGCGCGCGGTGTGCA 1754

RESULT 8
US-09-025-691-2
; Sequence 2, Application US/09025691
; Patent No. 6069299
; GENERAL INFORMATION:
; APPLICANT: Broadway, Roxanne M.
; APPLICANT: Hartman, Gary E.
; TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
; TITLE OF INVENTION: CHITINOLYTIC ENZYMES

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 14603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,691
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldman, Michael L.
 REGISTRATION NUMBER: 30,727
 REFERENCE/DOCKET NUMBER: 19603/20120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1304
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1294 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-025-691-2

Query Match 5.1%; Score 62.4; DB 3; Length 1294;
 Best Local Similarity 42.5%; Pred. No. 9.1e-05;
 Matches 389; Conservative 0; Mismatches 523; Indels 3; Gaps 1;

Qy	243	GGCGGCGATCGAGCGGCGCCGCTGCGCGCCGACGCTTGGGGGAGCAATCACTACAC	302
Db	197	GGTACGACCTTACCTTCCGACCCCGCGCGCCCTTCCACCGCGCCCTCCACCG	256
Qy	303	CGACTGGCGCGGACCAATTTCTATCGCGCGCTGCGCAGCTACCAAGGCGCCCAAGCG	362
Db	257	CAGGGGCGGCTACCGCGCCCTTCAACCGCGCGCTGCGCGCCCTTCCGGGCTCGCCCT	316
Qy	363	CATCGGCGATGAGTTCGACCACTCAATCTGCACTTCCGCGCGCAGCTCGAGAAAGCCCT	422
Db	317	CACCGCGCGCGACCGCGCGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT	376
Qy	423	ACCGGCGCTGATTTGTCGACATCAAGCCCTCGATGTGATGCGACCACTCAAGTC	482
Db	377	ACCGGCGCGACCGCGTACCGCTTACGGAACCTTCAACAGCGCGCGCGCTGCGAGAC	436
Qy	483	GCTCGAAGCAGAGCTGATCCGCGAAGGCGCGCGCTGTGAGCTGCGCGCGCGCGCG	542
Db	437	CCTCGCGAGCTCCGAGCGCTTACGACATCATGCGCGCTTCTTCCGCGCGCGCGCG	496
Qy	543	CTCGCGCGCTGCTCATGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	602
Db	497	CACGCGCGGAGATACCTTCAACCTCGACCTGCGCGCGCGCGCGCGCGCGCGCGCG	556
Qy	603	TGCGATGATCCGCGAGTCCGCAATCTGTTCCCTTCTGAGAGCTGAGCACTGGAC	662
Db	557	GCAGTTCGCGCGCGACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	616
Qy	663	CTGGTTCGAGCGGAGTCAACACCGAGCGCGCGCAATCCGCTCAACACCGCATCGT	722
Db	617	CGCGCGCGAGAGGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	673
Qy	723	GCAATCCGCGGACATCTTTCGCTCAACACTTCCGATGATCTTTCGCGCTACTACCG	782
Db	674	CGACGACACTACGCGCTGATGAGGAGTACGCGCTTCAACGCGGCTGCACTGACCTGGA	733

Qy	783	GCTGAGCGGACGCGCTGTCGCGACCATGTCAGCGCGCGCTCGACATCTGGAGAA	842
Db	734	GAAAGGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	793
Qy	843	GAAAGGCGGTCGATCGCGCGCGCTGAGTGAAGCGCGCGCGCTGCAAGGA	902
Db	794	GAGCGCGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	853
Qy	903	CATCGCGTACGAGCTCAAGAGATGTCACCGCGAGTGGAGCTGTAAGTCCGCTCTT	962
Db	854	GTACTTCAAGAGCGCGCTGTCAGCAAGACTTCTGACCGCGCGCGCGCGCGCG	913
Qy	963	CGGCTATGCGCACTCTTCCGCGCGCTGTCGCACTTCACTTCACTTCACTTCACTT	1022
Db	914	CACGCGCGCTGATCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	973
Qy	1023	GCTGCGGAGGACATGACACCGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCG	1082
Db	974	CCTCACGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1033
Qy	1083	GCTGATGCTGCGGAGGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1142
Db	1034	CGGTGTCCCGCGCTCCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1093
Qy	1143	CGTGGGAGAGACCGG 1157	
Db	1094	CGAGCGCTGAGCTG 1108	

RESULT 9
 US-09-475-515-54
 Sequence 54, Application US/09475515A
 Patent No. 6602705
 GENERAL INFORMATION:
 APPLICANT: BARNETT, Susan
 APPLICANT: ZUR MEGEDE, Jan
 APPLICANT: SRIVASTAVA, Indresh
 APPLICANT: LIAN, Ying
 APPLICANT: HARTOG, Karin
 APPLICANT: LIU, Hong
 APPLICANT: GREER, Catherine
 APPLICANT: SELBY, Mark
 APPLICANT: WALKER, Christopher
 TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
 FILE REFERENCE: 1621.002
 CURRENT APPLICATION NUMBER: US/09/475,515A
 CURRENT FILING DATE: 1999-12-30
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 54
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: gp120.modus4
 US-09-475-515-54

Query Match 5.0%; Score 60.6; DB 4; Length 1599;
 Best Local Similarity 42.6%; Pred. No. 0.00023;
 Matches 434; Conservative 0; Mismatches 579; Indels 6; Gaps 2;

Qy	196	CGAAGTACGCGATGCTATCGACCAACAAGCCGACGATTTGGCGCGCGATGAC	255
Db	364	CCCTGTGTGTGATACCTGATGACCGACGAGCTGACCGCGCGCGCGCGCGCGCG	423
Qy	256	GGGCGCGACCGCTGCGCGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCG	315
Db	424	AGCACGAGGCGGACCAACAGCACGACGCGCGCGCGCGCGCGCGCGCGCGCGCG	483
Qy	316	GCAATTTTATCGCGCGCGCGCGCGCGCT---GACCAAGGCGCGCGCGCGCGCG	372
Db	484	AGCTGGAGAGAGATGCTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	543

QY 1033 GACATCGACACCGAGCTGAAGCCCGCATGTGTCTCCATGAGCCGATGTGATGCTG 1092
DB 1201 TGCACACACGACGAGCTGTTCAACAGCACCTGGAAATCATCAGAGAGGTGAACAAGACC 1260
QY 1093 CCGAGGAGCATGCCCGGTGCGGCGGCTATTCGGAGCAAGACATCTGTATCTGCGGGAG 1152
DB 1261 AAGAGAAAGACACCATCTCTGCGGCTCGCATCCGCAATCTCAACATGTGGCAG 1320
QY 1153 GACGCTCCGAGACATCACCGGCTTCCGTTGCTCCGAAACACACCATCATTCGGCA 1211
DB 1321 GAGTGGGCAAGGCGCATGTAGCGCCCGCCCATCCGCGGCGAGATCAAGTGACAGCA 1379

RESULT 11

US-09-475-515-57
; Sequence 57, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; US-09-475-515-57

Query Match 5.0%; Score 60.6; DB 4; Length 2112;
Best Local Similarity 42.6%; Pred. No. 0.00025;
Matches 434; Conservative 0; Mismatches 579; Indels 6; Gaps 2;

QY 196 CCGAAGTACGGATGTCTATCCACCAACAGCCAGCATTTCCGCGCGCATCCAG 255
DB 364 CCCCTGTGTGATACCTGTAACATGACCAAGCTGACCGGAGCAACAGCGCAAC 423
QY 256 GCGGCGCAGCCCTGCGCGCGGAGCTTCCGAGCAACATCACTACCGATGGCGCGC 315
DB 424 AGCACCAGGCGGACCAACAGCAACAGCGGACCAACAGCAACAGCAACAGC 483
QY 316 GACAAATTTCTATCGCGCGGCGGAGCT--GACCAAGGCGCGCAAGCGCATTCGCATC 372
DB 484 AGCTGGAGAGATGCGGAGGCGGAGATCAAGAACTGAGCTTCAACATCAACACAGC 543
QY 373 GAGTTGACCACTCATCTGCACTTCCGCGCGGAGCTGAGAGAGCCCTTACCGGCGTC 432
DB 544 GTGCGCGAGCAAGGTGAGAGAGTACAGCTGTTCTAAGCTGAGCGTGTGCCATC 603
QY 433 GACTTCGTGACATGACGAGCCCTGATGTGATGCGGACCATCAAGTCCGTGCAAGAG 492
DB 604 GACAAAGCAACGCGGAGCTGATCCGCTGATCAACTGAAACAGAGCTGATCAACAGCGC 663
QY 493 CAGAAAGTGTATCCGGAAGCGCGCGGTGTGTGAGCTGCGCGCGCGCTGCGGCGCT 552
DB 664 TCGCCCAAGGTGAGCTTCAAGCGCATCCCATCTCACTAGCGGCGCGCGCGCTTCCGC 723
QY 553 GGCATCAAGCGCGGCTGCGGAGATGAGTGGCGATGCCACCAACATCGATGATC 612

DB 724 ATCTGAAGTGAAGAGACAAAGTTCAACGCGCACCGGCCCTGCAAGAACGTGAGCAC 783
QY 613 CCGGAGATCGCCAAATCTTCCCTCTTGTGAGCTGATGAGACACTGACCTGTTCCAG 672
DB 784 GTGCGATCACACACGAGCATCGCCCGCTGTGAGACACCGCTCTGTGAACGAGC 843
QY 673 TCGGCGATCAACACGAGCGGCGGCAATCCGATCCGATCCGATGTCATTCGCGC 732
DB 844 CTGGCGAGAGAGATGTGTGCTGCTCCGAGAACTTCACTGACAAAGCCCAAGACATC 903
QY 733 GACATCTTTGCTCAACACCTTCCGATGATCTTCCGCTACTACACCGCGCTGAGCGC 792
DB 904 ATCGTGACGTGAAGAGATCGGTGAGATCAACTGATCATCCGCCCAACAAACAGCGT 963
QY 793 ACGTGTCTGTGACATGTGTGATGATGACCGCACCTCGACATCTGGAGAGAACGTGGC 852
DB 964 AAGACATTCACATCGGCGCGCGCTTCTAAGCCACCGCGGAGCATCATTCGCGCAG 1023
QY 853 GTGCAATCGCGCGGCTGAGCTGATCAAGCGCGGCGGCGGCTGCAAGGACATCGGCATC 912
DB 1024 ATCCGCGCAGGCGGCTGATGACATGACAGCAAGGCACTGAGACTACACCTCGAGCAGATC 1083
QY 913 GAGCTCAAGAGATGTATCCGAGAGTGGAGCTGTGAGTACCGCTCTTCCGCTATGAGC 972
DB 1084 G---TGAAGAGCTCGCGGAGCAGTTCGGCAACAAAGACATCATCTTCAACAGCAGC 1140
QY 973 CACTCTTGTGGGCTGTGTGCTCACTAATGAGTCCGAGGCGCGGCTGAGAGCTGCGCAG 1032
DB 1141 AGCGCGGCGGAGCGCGGAGATGTGTTCCAGCTTCACTGCGGCGGAGGATCTTCTAC 1200
QY 1033 GACATCGACACCGAGCTGAAGCCCGGAGTGTGTCTCATAGAGCCGATGTGATGCTG 1092
DB 1201 TGCACACACGACGAGCTTTCACAGCACTGGAACATCAACGAGAGGTGAACAAGACC 1260
QY 1093 CCGAGGAGCATGCCCGGTGCGGCGGCTATTCGGAGCAAGACATCTGTATCTGCGGGAG 1152
DB 1261 AAGAGAAAGACACCATCATCTCTGCGGCTCGCATCCGCAATCATCAAGTGGCAG 1320
QY 1153 GACGCTCCGAGACATCACCGGCTTCCGTTGCTCCGAAACACACCATCATTCGGCA 1211
DB 1321 GAGTGGGCAAGGCGCATGTAGCGCCCGCCCATTCGCGGCGAGATCAAGTGACAGCA 1379

RESULT 12

US-09-475-515-58
; Sequence 58, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: gp140TM.modusa
; US-09-475-515-58

Query Match 5.0%; Score 60.6; DB 4; Length 2181;
Best Local Similarity 42.6%; Pred. No. 0.00025;
Matches 434; Conservative 0; Mismatches 579; Indels 6; Gaps 2;

```
QY 196 CGCAAGTACGCGATGTCATCGACCAACAACCGCCAGCATTTGCGCGGATGAC 255
DB 364 CCCGTGTGCGTGAACCTCGAATGACGACGACAGTGAACCGGACCAACAGGACCAAC 423
QY 256 GCGGCGCAAGCCCTGGCGCCGAGCTTGGCGCAACATCACTACACCGACTGGCGCGC 315
DB 424 AGCACCGCGGACCAACAGACGACGACCAACAGCACCAAGCACCAAGACGACGAC 483
QY 316 GACAATTTATGCGCGCGTGGCGGAGCT---GACCAAGGCGCGCAAGGCGCATCGGATC 372
DB 484 AGCTGGAGAAATGCTCCGAGGCGGAGATCAAGATTCAGCTTCAACATCAACACAGC 543
QY 373 GAGTTGACCAAGTCATCTGACTTCCGCGCGGACGTCGAGGAGCCCTACCGGCGTC 432
DB 544 GTGGCGGACAAAGGTGAGAAAGAGTACAGCTGTCTTCAAGCTGGACGTGGTCCATC 603
QY 433 GACTTGTGACATCAGCGACGCTCGATGTGATGCGCACCATCAAGTGGCTGAAAG 492
DB 604 GACAACGACAAAGCGACGCTACCGCTGATCACTGCAACACAGCGTATCACCGAGCC 663
QY 493 CAGAAGCTATCGCGGAAAGCGCGCGTGTGATGATCGGCGCGCGCGCTCGCGGCT 552
DB 664 TGCCCCAAGGTGAGCTTGCAGCCCATCCCATCTCACTGCGCGCGCGCGCTTCCGC 723
QY 553 GCCATCAAGGCGCGCGTGCAGCATGATGAGTGCATCGCCACCAACATGCGATGATC 612
DB 724 ATCTGGAAGTGAAGAGCAAGAAAGTTCAAGGACCGCGCGCTGCAAGAACTGAGAC 783
QY 613 CGCGAGATCGCCAAATGCTTCCCTTGTGAGCTGATGACACCTGAGCTGGTTCCAG 672
DB 784 GTGCACTGACACCAAGCGGACCGCGCGTGTGAGCTGATGAGCTGATGAGCTGAGC 843
QY 673 TCGGGATCAACAACGAGCGGCGGCAACATCGGCTCAACAAGGCGATCGCATCGGCG 732
DB 844 CTGGCCGAGAGAGATGCTGCTGCTCGGAGAACTTCAACGACCAAGCGCAAGACATC 903
QY 733 GACATCTTTCGCTCAACACTTCCGATGATCTTCCGCTACTTCAACCGCGCTGAGCGC 792
DB 904 ATGTGAGCTGAACGATCGGTGAGATCACTGCACTCGCCCAACAAACAGCGCT 963
QY 793 AGCGTGTTCGCAACATGTCATGACGCGACCTCGACATCTGGGAGAAAGAGTGGCC 852
DB 964 AAGAGCATCCACATCGGCGCGCGCGCTTCTTACGCGACGACATCATCTGGGAGC 1023
QY 853 GTGCAATCGCGCGCGGCTCGAGCTGATCAACCGGCGCGCGCTGCAAGGACATCGCATC 912
DB 1024 ATCCGCGAGGCGCACTGCAACATCAAGAGGCACTGCAACCAACCTTGAAGCATC 1083
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DB 1084 G---TGAGAAAGCTGGCGGAGAGTTCGCGCAACAAGACATCACTTCAACAGAGC 1140
QY 973 CACTCTTTCGCGCTGCTGCTGCTCACTACTACGTCGCGAGGCGCGTGGAGCTCGCGAG 1032
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QY 1093 CCGGAGGAGTGCCTGGTGCCTGGGCTATTCGCGAGCAGACATCTGATCTGCGGAG 1152
DB 1261 AAGAGAAAGACATCATCTGCTGCTGCGCATTCGCGAGTCAATCAAGTGGAG 1320
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RESULT 13
US-09-475-515-64
Sequence 64, Application US/09475515A

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/ Patent No. 6602705
/ GENERAL INFORMATION:
/ APPLICANT: BARNETT, Susan
/ APPLICANT: ZUR MEGEDE, Jan
/ APPLICANT: SRIVASTAVA, Indresh
/ APPLICANT: LIAN, Ying
/ APPLICANT: HARTOG, Karin
/ APPLICANT: LIU, Hong
/ APPLICANT: GREER, Catherine
/ APPLICANT: SELBY, Mark
/ APPLICANT: WALKER, Christopher
/ TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
/ FILE REFERENCE: 1621.002
/ CURRENT APPLICATION NUMBER: US/09/475,515A
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 64
/ LENGTH: 2634
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: gp160.modus4
US-09-475-515-64
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Query Match 5.0%; Score 60.6; DB 4; Length 2634;
Best Local Similarity 42.6%; Pred. No. 0.00026;
Matches 434; Conservative 0; Mismatches 579; Indels 6; Gaps 2;

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DB 364 CCCGTGTGCGTGAACCTCGAATGACGACGACAGTGAACCGGACCAACAGGACCAAC 423
QY 256 GCGGCGCAAGCCCTGGCGCCGAGCTTGGCGCAACATCACTACACCGACTGGCGCGC 315
DB 424 AGCACCGCGGACCAACAGACGACGACGACCAACAGCACCAAGCACCAAGACGACGAC 483
QY 316 GACAATTTATGCGCGCGTGGCGGAGCT---GACCAAGGCGCGCAAGGCGCATCGGATC 372
DB 484 AGCTGGAGAAATGCTCCGAGGCGGAGATCAAGAACTGAGCTTCAACATCAACACAGC 543
QY 373 GAGTTGACCAAGTCATCTGACTTCCGCGCGGACGCTGAGGAAAGCCCTACCGGCGTC 432
DB 544 GTGGCGGACAAAGGTGAGAAAGAGTACAGCTGTCTTCAAGCTGGAAGTGGTCCATC 603
QY 433 GACTTGTGACATCAGCGACGCTCGATGTGATGCGCACCATCAAGTGGCTCGAAGAG 492
DB 604 GACAACGACAAAGCGGACGCTTACCGCTGATCACTGCAACCAAGGCTGATCAACCGAGCC 663
QY 493 CAGAAGCTATCGCGGAAAGCGCGCGTGTGATGATGCGGCGCGCGCGCTTCCGAGCT 552
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QY 613 CGCGAGATGCGCAAAATGCTTCCCTTGTGAGCTGATGAGAACCTGAGACTGGTTCAG 672
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DB 904 ATGTGAGCTGAAGAGATGCTGAGATCACTGATCGCGCGCGCGCAACAAACAGCGCT 963
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US-09-475-515-73
; Sequence 73, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 4766
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; ;
; OTHER INFORMATION: gp160, modUS4, gag, modSF2
; ;
; US-09-475-515-73

Query Match 5.0%; Score 60.6; DB 4; Length 4766;
Best Local Similarity 42.6%; Pred. No. 0.00029;
Matches 434; Conservative 0; Mismatches 579; Indels 6; Gaps 2;

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RESULT 15

US-09-025-691-4
; Sequence 4, Application US/09025691
; Patent No. 6069299
; GENERAL INFORMATION:
; APPLICANT: Broadway, Roxanne M.
; APPLICANT: Harman, Gary E.
; TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
; TITLE OF INVENTION: CHITINOLYTIC ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester

GenCore version 5.1.6
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OM nucleic - nucleic search, using 6w model

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Maximum Match 100%
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- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	981.6	81.0	1215	US-10-251-078-1	Sequence 1, Appl1
2	981.6	81.0	1215	US-10-251-078-17	Sequence 17, Appl1
3	978.4	80.7	1215	US-10-251-078-9	Sequence 9, Appl1
4	976.8	80.6	1212	US-10-251-078-11	Sequence 11, Appl1
5	976.8	80.6	1212	US-10-251-078-13	Sequence 13, Appl1
6	976.8	80.6	1215	US-10-251-078-15	Sequence 15, Appl1
7	975.2	80.5	1212	US-10-251-078-21	Sequence 21, Appl1
8	973.6	80.3	1212	US-10-251-078-19	Sequence 19, Appl1
9	75.4	6.2	2733	US-10-437-963-88003	Sequence 88003, A
C 10	73.4	6.1	1262	US-10-425-115-109294	Sequence 109294, A
11	69.8	5.8	1483	US-10-437-963-38426	Sequence 38426, A
12	69.6	5.7	9025608	US-10-156-761-1	Sequence 1, Appl1

13	68.8	5.7	65140	17	US-10-203-295-1	Sequence 1, Appl1
14	68.8	5.7	125401	17	US-10-203-295-35	Sequence 35, Appl1
C 15	68.6	5.7	1169	17	US-10-437-963-57011	Sequence 57011, A
16	68	5.6	834	17	US-10-156-761-4932	Sequence 4932, Ap
17	68	5.6	1212	18	US-10-411-910A-222	Sequence 222, Ap
C 18	67	5.5	2569	17	US-10-437-963-88004	Sequence 88004, A
19	67	5.5	4512	15	US-10-156-761-2222	Sequence 2222, Ap
C 20	67	5.5	9025608	15	US-10-156-761-1	Sequence 1, Appl1
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22	66	5.4	2037	15	US-10-228-063-48	Sequence 48, Appl1
23	65	5.4	573	15	US-10-156-761-3931	Sequence 3931, Ap
24	65	5.4	2026	17	US-10-437-963-32278	Sequence 32278, A
C 25	65	5.4	2052	17	US-10-282-122A-11731	Sequence 11731, A
26	65	5.4	2649	17	US-10-437-963-112	Sequence 112, App
C 27	64.6	5.3	1752	18	US-10-411-910A-234	Sequence 234, App
C 28	64.4	5.3	2960	17	US-10-437-963-34365	Sequence 34365, A
29	64	5.3	1516	17	US-10-437-963-29365	Sequence 29365, A
30	64	5.3	2364	17	US-10-473-687-3	Sequence 3, Appl1
31	63.6	5.2	690	13	US-10-006-922-27	Sequence 27, Appl1
32	63.6	5.2	690	14	US-10-081-864-19	Sequence 19, Appl1
33	63.6	5.2	1248	18	US-10-411-910A-220	Sequence 20, App
34	63.6	5.2	1311	18	US-10-411-910A-200	Sequence 2, Appl1
35	63.6	5.2	9546	16	US-10-463-074-2	Sequence 271, App
36	63.4	5.2	1083	16	US-10-260-238-271	Sequence 412, App
37	63	5.2	18435	15	US-10-156-761-412	Sequence 15103, A
38	63	5.2	100000	15	US-10-156-761-15103	Sequence 5241, Ap
39	62.8	5.2	1053	15	US-10-156-761-5241	Sequence 176, App
40	62.8	5.2	9785	16	US-10-359-120-176	Sequence 266, App
41	62.6	5.2	1377	18	US-10-411-910A-266	Sequence 4461, App
42	62.6	5.2	1479	15	US-10-156-761-4461	Sequence 209, App
43	62.6	5.2	1758	18	US-10-411-910A-209	Sequence 2, Appl1
44	62.4	5.1	1294	9	US-09-748-033-2	Sequence 7186, Ap
45	62.4	5.1	1335	15	US-10-156-761-7186	

ALIGNMENTS

RESULT 1
US-10-251-078-1
; Sequence 1, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
; APPLICANT: Schmuck, Rainer
; APPLICANT: Kratzsch, Peter
; APPLICANT: Kenkies, Janet
; APPLICANT: Weisser, Harald
; TITLE OF INVENTION: Variants of an Erythrina-type creatinase
; FILE REFERENCE: 20981 EP
; CURRENT APPLICATION NUMBER: US/10/251.078
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Erythrina sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-251-078-1

Query Match 81.0%; Score 981.6; DB 15; Length 1215;

Best local Similarity 88.1%; Pred. No. 8.9e-254; Matches 1068; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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Db 1 ATGACTGACGACATGTTGCAAGTATGACAAACGCGCAAGATATTCGCG 60
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Qy 61 TTTTCGATGCGGAGATGACCCGCGCCAAAACGACGTTCCGCGCTGATGCGCAAGAC 120

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Qy 121 AATGTCGATGCGGCGCTGTTCACCTCTTATCACTGATCACTACTATTCGCGCTG 180
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; Sequence 17, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
; APPLICANT: Schmuck, Rainer
; APPLICANT: Kraltsch, Peter
; APPLICANT: Kenkies, Janet
; APPLICANT: Weisner, Harald
; TITLE OF INVENTION: Variants of an Erwinia-type creatinase
; FILE REFERENCE: 20981 BP
; CURRENT APPLICATION NUMBER: US/10/251,078
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variant CTGc2
; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-251-078-17
Query Match 81.0%; Score 981.6; DB 15; Length 1215;
Best Local Similarity 88.1%; Pred. No. 8.9e-254;
Matches 1068; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
Qy 1 ATGACTGACGATGTTGACGCTGATGAAATGGACAAAGCGGAGAAAGATTATTCGCG 60
Db 1 ATGACTGACGATGTTGACGCTGATGAAATGGACAAAGCGGAGAAAGATTATTCGCG 60
Qy 61 TTTTCGATGCGGAGATACCCGCGCGCAACAGCTTCCGCGCTGATGGCGCAAG 120
Db 61 TTTTCGATGCGGAGATACCCGCGCGCAACAGCTTCCGCGCTGATGGCGCAAG 120
Qy 121 AATGTCGAGGCGGCTGTTCACCTCTTATCACTGATCACTACTATTCGCGCTG 180
Db 121 GAGTCGACGCTGCGCTGTTCACCTCTTATCACTGATCACTACTATTCGCGCTG 180
Qy 181 TACTGCTATTTGGAGCGCAAGTACGGCATGCTCATGACCAACAGCCGACAGAGATT 240
Db 181 TACTGCTATTTGGAGCGCAAGTACGGCATGCTCATGACCAACAGCCGACAGAGATT 240
Qy 241 TCGGCGCGGATCGAGTGGCGGCTGAGCCCTGCGCGCGGAGCTTGGCGCAACATCACTAC 300
Db 241 TCGGCGCGGATCGAGTGGCGGCTGAGCCCTGCGCGCGGAGCTTGGCGCAACATCACTAC 300
Qy 301 ACCGACTGGCGCGCGCAATTTTATTCGCGCGGCGCGCAGCTGAACAAGCGCGCAAG 360
Db 301 ACCGACTGGCGCGCGCAATTTTATTCGCGCGGCGCGCAGCTGAACAAGCGCGCAAG 360
Qy 361 CGCATCGGATCGAGTTGCAACACGTCATCTGATCTTCCGCGCGCACTCGAGAGACC 420
Db 361 CGCATCGGATCGAGTTGCAACACGTCATCTGATCTTCCGCGCGCACTCGAGAGAGCG 420
Qy 421 CTACCGGCGGCTGCACTTCGTCATCAGCGAGCCCTGATGAGTGGCAACATCAAG 480
Db 421 CTGCGCGGCGGCTGAGTTGCTGATTCGATCAACCTGATGAGTGGCAACGCTCAAG 480
Qy 481 TCGCTCGAAGACAGAAAGCTGATCCGGAAGCGCGCGGCTGTGATCGTCGCGCGCG 540
Db 481 TCGCTCGAAGACAGAAAGCTGATCCGGAAGCGCGCGGCTGTGATCGTCGCGCGCG 540

Dp	481	TCGGCTGAAAGACAGAAAGCTGATCCGCGAGGGGTGCCGATATCTGCACGTCGGCGGTGCC	540
Qy	541	GCCTGCGCGGCTGGCCATCAAGGCCCGGCGTCCCGAGCATGAAGTGGCGATTCGCACACC	600
Dp	541	GCCTGCGTTCGCGCGGTCAAGGCCCGGCGTTCGCGAGCAGAGAGTGGCATTCGCACACC	600
Qy	601	AATGGGATGATATCCGGGAGATTCGCCAAATGTTTCCCTTTGTGGAAGTGTGACACCTGG	660
Dp	601	AATGGGATGATATCCGGGAGATTCGCCAAATGTTTCCCTTTGTGGAATGTGTGACACCTGG	660
Qy	661	ACCTGATTCAGATCGGGGATCAACCCGAGGGGGGCAAAATCCGGTACCAACCGGCATC	720
Dp	661	ACCTGATTCAGATCGGGGATCAACCCGAGGGGGGCAAAATCCGGTACCAACCGGCATC	720
Qy	721	GTGCAATCCGGGCGACATCTTTTCGTCAACAACCTTCCGATGATTTTCGGCTACTCAACC	780
Dp	721	GTGCAATCCGGGCGATCTCTGTCCGTCAACAAGTTTCCGATGATTTTCGGCTACTCAACC	780
Qy	781	GGCGTGGAGCGCACGCTGTTCTTGCCAGCATTGTGCATGACGCCAGCCTCGACATCTGGAG	840
Dp	781	GGCGTGGAGCGCAACCTGTTCTGTGACACAGTCGACGATGCCAGCCTTGCACACTGGAG	840
Qy	841	AAGAACGTGGCGCGTGCATCGCGCGGGGCTCGAGCTGATCAAGCCGGGGGCGCGCGTGCAG	900
Dp	841	AAGAACGTGCGCGGTGCATCGCGCGGGGCTCGAATCTCATCAAGCCGGGGTGCAG	900
Qy	901	GACATCGGCATCGAGCTCAACGAGATGTACCGCGAGTGGGACTTGTCTGAAGTACCGCTCC	960
Dp	901	GATATCGGCATCGAATCAACGAGATGTACCGGGAGTGGGATCTGTGAAGTACCGCTCC	960
Qy	961	TTTCGGCTATGGCCATCTCTTGGGGGTGTGTCCTACTACGATGCGTGGAGGCCGGCGTG	1020
Dp	961	TTTCGGCTATGGCCATCTCTTGGGGGTGTGTCCTACTACTACGATGCGGAGGCCGGCGTG	1020
Qy	1021	GAGCTGCGCGAGGACATCGACACGAGGCTGAAAGCCCGGATGATGTGTCTCATGGAGGCG	1080
Dp	1021	GAGCTGCGCGAGGACATCGATACGCTGTCTGAGCCCGGATGATGTGTCTCATGGAGGCG	1080
Qy	1081	ATGTGATGATCTGCGCGGAGGAGATGCGCGGATGCGCGGCTATTCGAGACAGACATCTCTG	1140
Dp	1081	ATGTGATGATTTTTCGAGAGAGGGGCTCCGGCGGGCGGGCTACCGGAGACAGACATCTCTG	1140
Qy	1141	ATCGTCGGGGAGAGCGGTGCGAGAACATCACCGGCTTCCGTTGATTCGGAAACACAC	1200
Dp	1141	ATCGTCGGGGAGAGCGGCGAGAGAACATTAACGGATTTCCCTTCGGGCTGAGACACAC	1200
Qy	1201	ATCATCCGCAAC 1212	
Dp	1201	ATCATCCGCAAC 1212	

```

RESULT 3
US-10-251-078-9
Sequence 9, Application US/10251078
Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixian
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kemmlies, Janet
APPLICANT: Weisber, Harald
TITLE OF INVENTION: Variants of an Ewln1a-type creatinase
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251, 078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1215
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:

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; OTHER INFORMATION: Description of Artificial Sequence:variant C11M24
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (1)..(1215)
US-10-251-078-9

```

Query Match	80.7%;	Score 978.4;	DB 15;	Length 1215;
Best Local Similarity	88.0%;	Pred. No. 6.5E-253;		
Matches 1066; Conservative	0;	Mismatches 146;	Indels 0;	Gaps 0

QY	1	AATGACTGACGAACTGTTGACGCGATGAATGGCAACAACGGCCAGAAAGATTTATCCGCG	60
Db	1	ATGACTGACGAACTGTTGACGCGATGAATGGCAACAATGTTGAAAGAAATTTCCCC	60
QY	61	TTTTGGAGATCCGAGATGACCCGGCCGCAAAAGACGTTTCGGCTGGATGGCCAGAAC	120
Db	61	TTTTCCGATGCGAGATGACCGGGCCGCAAGATGACGTCGGCGCTGGATGGCCGAAAC	120
QY	121	AATGTGAAAGGCGCGTGTTCACCTTTATCATGTGATCAACTATATTCGGGCTGGCTG	180
Db	121	GACGTGACGCTGCGCTGTTCACCTTCATCATATGATCAACTATATCTTGAATTCCTG	180
QY	181	TACTGCTATTTTGGAGCGCAAGATGAGGATGATGACCAACAACAAGCCACGACGATT	240
Db	181	TACTGCTATTTTGGCGCGCAAAATACGAGATGATGATGACCAAGAACATGCAAGACATC	240
QY	241	TGGCGCGGAGATGACGCGCGCCAGCCCTTGGCGCCGCAAGCTTTGGGCGCAACATACCTAC	300
Db	241	TGGCGCGGAGATGATGGCGGTCAGCCCTTGGCGCCGCTTGAAGCTTGGCGCAACATCACTAT	300
QY	301	ACCGACTGGCGCGCGGCAAAATTTCTATTCGCGCGCTGGGCGAGCTGACCAAGGGCGCAAG	360
Db	301	ACGGACTGGCGCGCGGCAAACTTCTATCAAGGCGCTGGCGCAACTCACCCCGGCGCAAG	360
QY	361	CGCATCGGCACTGACGTTTGCACCAACGCTCAATCTGCATTCCGCGCGCAGCTCGAGAAAGCC	420
Db	361	CGCATCGGATATGCAATTCGATTCACGTTGACCTTGCCTCGCAGACGCTCGAAAGAGCG	420
QY	421	CTACCGGCGCTGCACTTTCGTGACATCAAGCCAGCCCTCGATGTGATGCGCACCATCAAG	480
Db	421	CTGCGCGGCGTGCAGATTGCTGCAATTCGGTCAACGTCGATGTGATGCGCACGGTCAAG	480
QY	481	TGCGTTCGAAAGACAAAGACTGATCCGCGGAAGCGCCCGCTGTGTGAAGCTCGGCGCGG	540
Db	481	TGCGTTCGAAAGACAAAGACTGATCCGCGAGGCTGCCGCTATTCGCAACGTCGCGCGGTGCC	540
QY	541	GCGTGGCGGCTGCCATCAAGCGCGGCGTCCCGGAGCAATGAAGTGGCGAATCCGCAACAC	600
Db	541	GCGTGGCTTGGCGCGCTGCAAGCGCGGCGTTCGAGAGCAAGAGGTGGCGAATCCGCAACAC	600
QY	601	AATGCGATGATTCGCGGAGATGCGCAAAATTCGTTCCCTTCGTGGAGCTGATGGAACCTGG	660
Db	601	AATGCGATGATTCGCGGAGATGCGCAAGTCTTCCTTCGTGGACTGATGGAACCTGG	660
QY	661	ACCTGGTTCAGTGGGAGCATCAACCGAGCGGCGCAAAATCCGGTCAACAACCGCATC	720
Db	661	ACCTGGTTCAGTGGGAGCATCAACAACCGCGGCGCCCAAAATCCGGTGAACAACCGCATC	720
QY	721	GTCGAATTCGGCGGACATCTTTTCGTCAACACTTTCGCCGATATCTTGGGCTATCTACACC	780
Db	721	GTCGAATTCGGCGGAGATCTCTGCTCAACAGTTTCGCCGATATCTTGGGCTATCTACACG	780
QY	781	GCGCTGGAGCGCAAGCTGTTCTTGGCAACCATGTCGATGACGATGCGACGCTTGAACCTTGGAG	840
Db	781	GCGCTGGAGCGCAAGCTGTTCTTGGCAACCATGTCGATGACGATGCGACGCTTGAACCTTGGAG	840
QY	841	AAGAAGCTGGCGCTGCACTGCGCGCGGCTCGAGCTGATCAAGCCGGGCGCGCGCTGCAAG	900
Db	841	AAGAAGCTGGCGCTGCAACCGCGCGGCTCGGAATCACTCAAGCCGGGTCGCGCTGCAAG	900
QY	901	GACATTCGCGCATCGAGCTCAACGAGATGTATCGCGAGTGGGACCTTCTGTAAGTACCGCTTC	960
Db	901	GATATTCGCGCATCGAATCAACGAGATGTATCGCGAGTGGGATCTCTGAAGTACCGCTTC	960

QY 961 TTGGGCTATGCGCACTCTTCCGGCGTGTCTGTGCACTACTACGCTGCGGAGCGCGCGT 1020
DB 961 TTGGGCTATGCGCACTCTTCCGGCGTGTCTGTGCACTACTACGCTGCGGAGCGCGCGT 1020
QY 1021 GAGCTCGGAGGACATCGACACCGAGCTGAAGCCCGGCAATGTGTCTTCATGAGCGG 1080
DB 1021 GAACTCGGAGGACATCGATACCGGTCTGTGCAAGCCCGGCAATGTGTCTTCATGAGCGG 1080
QY 1081 ATGTGATGCTGTGCGGAGGCAATGCCGCTGCGGCGGCTTATGCGAGCAGCATCTTG 1140
DB 1081 ATGTGATGCTGTGCGAAGGCGCTCCCGGCGGCGGCTTATGCGAGCAGCATCTTG 1140
QY 1141 ATGTGCGGAGGAGCGGTGCGGAGCATCAGCGGCTTCCGTTCCGTCGCGAAGCAGCACC 1200
DB 1141 ATGTGCGGAGGAGCGGCGGAGCATCAGCGGATTCCTGATCCCTTCCGCGCTGAGCAAC 1200
QY 1201 ATCATCGGCAC 1212
DB 1201 ATCATCGGCAC 1212

RESULT 4
US-10-251-078-11
; Sequence 11, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
; APPLICANT: Schuck, Rainer
; APPLICANT: Kratzsch, Peter
; APPLICANT: Kenkies, Janet
; APPLICANT: Weisser, Harald
; TITLE OF INVENTION: Variants of an Erwinia-type creatinase
; FILE REFERENCE: 20981 EP
; CURRENT APPLICATION NUMBER: US/10/251,078
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variant CT2m3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1212)
US-10-251-078-11

Query Match 80.6%; Score 976.8; DB 15; Length 1212;
Beet Local Similarity 87.9%; Pred. No. 1.7e-252;
Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 ATGATGACGACATGTTGACGTGATGAATGAGCACAAGCGGAGAAATATTTCGCGG 60
DB 1 ATGATGACGACATGTTGACGTGATGAATGAGCACAAGCGGAGAAATATTTCGCGG 60
QY 61 TTTTGGATGCGGAGATGACCGCGCGCAAAAGAGTTGCGGCTGATGAGCAAGAC 120
DB 61 TTTTGGATGCGGAGATGACCGCGCGCAAAAGAGTTGCGGCTGATGAGCAAGAC 120
QY 121 AATGTGATGCGGCGGTGTTCACTTATCACTGATCAATCACTATTCGCGGTG 180
DB 121 AATGTGATGCGGCGGTGTTCACTTATCACTGATCAATCACTATTCGCGGTG 180
QY 121 GACGTGAGGCTGCGGTGTTCACTTATCACTGATCAATCACTATTCGCGGTG 180
DB 121 GACGTGAGGCTGCGGTGTTCACTTATCACTGATCAATCACTATTCGCGGTG 180
QY 181 TACTGCTATTTGCGAGCAGATGACGATGATGATGACGACCAAGCAGCAGATT 240
DB 181 TACTGCTATTTGCGAGCAGATGACGATGATGATGACGACCAAGCAGCAGATT 240
QY 241 TCGGCGGAGCAGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
DB 241 TCGGCGGAGCAGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

QY 301 ACCGACTGCGCGCGGACCAATTTCTATGCGCGCGTGTGCGGCACTGACCAAGCGCGCGG 360
DB 301 ACCGACTGCGCGCGGACCAATTTCTATGCGCGCGTGTGCGGCACTGACCAAGCGCGCGG 360
QY 361 CGCATCGGATGAGTGTGACCAAGCTGATCTGATCTGCGCGGCGGCGGCGGCGGCGGCGG 420
DB 361 CGCATCGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 CTACCGGCGGTGACTTGTGTGATCATCAGCCAGCCCTGATGTGATGTGAGCGCATCAAG 480
DB 421 CTGCGCGGCGGTGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 TCGCTCGAAGAGCAGAACTGATTCGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGG 540
DB 481 TCGCTCGAAGAGCAGAACTGATTCGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGG 540
QY 541 GCGTGGCGGCTGCGCATGAGCGCGCGTGCAGCATGAGAGTGGCGATCGCCACACC 600
DB 541 GCGTGGCGGCTGCGCATGAGCGCGCGTGCAGCATGAGAGTGGCGATCGCCACACC 600
QY 601 AATGCGGTGATCGCGGAGATGCGCAATGCTTCCCTTGTGAGCTGATGAGCAGCTGG 660
DB 601 AATGCGGTGATCGCGGAGATGCGCAATGCTTCCCTTGTGAGCTGATGAGCAGCTGG 660
QY 661 ACCGTGTTCCAGTGGGAGCATCAACCGAGCGCGGCGCAATCGCGTCAACCAACCGCATC 720
DB 661 ACCGTGTTCCAGTGGGAGCATCAACCGAGCGCGGCGCAATCGCGTCAACCAACCGCATC 720
QY 721 GTGCAATCGGCGGACATCTTGTGCTCAACCTTCCCGAGATCTTGGGCTACTACAC 780
DB 721 GTGCAATCGGCGGAGATCTTGTGCTCAACCTTCCCGAGATCTTGGGCTACTACAC 780
QY 781 GCGCTGAGCGGAGCTGTTGTGCGACCATGTGATGAGCGGCGGCTGACATCTGGAG 840
DB 781 GCGCTGAGCGGAGCTGTTGTGCGACCATGTGATGAGCGGCGGCTGACATCTGGAG 840
QY 841 AAGAAAGCGGCGGCGGAGCATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
DB 841 AAGAAAGCGGCGGCGGAGCATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 901 GACATCGGCGGAGCTGAGTGAAGATGACCGGAGTGAAGCTTGTGATGATGATGATGATG 960
DB 901 GATATCGGCGGAGTGAAGTGAAGATGACCGGAGTGAAGCTTGTGATGATGATGATGATG 960
QY 961 TTTGCGCTATGCGGCTGTTGCGGCGTGTGCGCATCTAAGTGTGCGGAGCGGCGG 1020
DB 961 TTTGCGCTATGCGGCTGTTGCGGCGTGTGCGCATCTAAGTGTGCGGAGCGGCGGCGG 1020
QY 1021 GAGCTGCGGAGGACATGAGCAGCGAGCTGAAGCGCGGCGGCGGCGGCGGCGGCGGCGG 1080
DB 1021 GAGCTGCGGAGGACATGAGCAGCGAGCTGAAGCGCGGCGGCGGCGGCGGCGGCGGCGG 1080
QY 1081 ATGTGATGCTGCGGAGGAGGAGTCCGCGTGCAGCGGCTTATGCGAGCAGCATCTTG 1140
DB 1081 ATGTGATGCTGCGGAGGAGGAGTCCGCGTGCAGCGGCTTATGCGAGCAGCATCTTG 1140
QY 1141 ATGTGCGGAGGAGGAGTGTGCGGAGCATCAAGCGGCTTCCGTTGCGGTGCGGAGACAC 1200
DB 1141 ATGTGCGGAGGAGGAGTGTGCGGAGCATCAAGCGGATTCCTTCCGCGCTGAGCAGAC 1200
QY 1201 ATCATCGGCAC 1212
DB 1201 ATCATCGGCAC 1212

RESULT 5
US-10-251-078-13
; Sequence 13, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin

APPLICANT: Schmuck, Rainer
 APPLICANT: Kratzsch, Peter
 APPLICANT: Kenkies, Janet
 APPLICANT: Weisner, Harald
 TITLE OF INVENTION: Variants of an Erwinia-type creatinase
 FILE REFERENCE: 20981 EP
 CURRENT APPLICATION NUMBER: US/10/251,078
 CURRENT FILING DATE: 2002-09-20
 NUMBER OF SEQ. ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 SEQ. ID NO. 13
 LENGTH: 1212
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: variant CT2m10
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1212)
 US-10-251-078-13

Query Match 80.6%; Score 976.8; DB 15; Length 1212;
 Best Local Similarity 87.9%; Pred. No. 1.7e-252;
 Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 ATGACTGACGACATGTTGACGTGATGAAATGSCAACACGCGGAGAAAGATTATTCGCGG 60
 DB 1 ATGACTGACGACATGTTGACGTGATGAAATGSCAACATGATGAGAAAGATTATTCGCGG 60
 QY 61 TTTTCGGATGCGGAGATGACCGCGCGCAACGAGCTTCGGGCGTGATGCGCAAGAAC 120
 DB 61 TTTTCGGATGCGGAGATGACCGCGCGCAACGAGCTTCGGGCGTGATGCGCAAGAAC 120
 QY 121 AATGTCATGCGCGCGCTGTTCACTCTTATCACTGATCACTAATATTCGCGGCTG 180
 DB 121 AATGTCATGCGCGCGCTGTTCACTCTTATCACTGATCACTAATATTCGCGGCTG 180
 QY 121 GACGTGACGCGCGCTGTTCACTCTTATCACTGATCACTAATATTCGCGGCTG 180
 DB 121 GACGTGACGCGCGCTGTTCACTCTTATCACTGATCACTAATATTCGCGGCTG 180
 QY 181 TACTGCTATTTGCGAGCGCAATGAGCGATGTCATGACACAGACATGCGACGACATC 240
 DB 181 TACTGCTATTTGCGAGCGCAATGAGCGATGTCATGACACAGACATGCGACGACATC 240
 QY 241 TCGGCGGCGATGACG 300
 DB 241 TCGGCGGCGATGACG 300
 QY 241 TCGGCGGCGATGACG 300
 DB 241 TCGGCGGCGATGACG 300
 QY 301 ACCGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 DB 301 ACCGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 301 ACGGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 DB 301 ACGGACTGCGCGCGCGCAATTTCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 361 CGCATCGGATGACG 420
 DB 361 CGCATCGGATGACG 420
 QY 421 CTACCGGCG 480
 DB 421 CTACCGGCG 480
 QY 421 CTGCG 480
 DB 421 CTGCG 480
 QY 481 TCGCTGGAAGACAGAGCTGATCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 DB 481 TCGCTGGAAGACAGAGCTGATCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 QY 481 TCGCTGGAAGACAGAGCTGATCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 DB 481 TCGCTGGAAGACAGAGCTGATCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 QY 541 GCGTGGCG 600
 DB 541 GCGTGGCG 600
 QY 601 AATGCGATGATCG 660
 DB 601 AATGCGATGATCG 660
 QY 661 AATGCGATGATCG 720
 DB 661 AATGCGATGATCG 720

QY 721 GTGCAATCGCGCGACATCTTTCGTCAACCTTCCGATGATCTTGCTACTACAC 780
 DB 721 GTGCAATCGCGCGACATCTTTCGTCAACCTTCCGATGATCTTGCTACTACAC 780
 QY 781 GCGCTGAGCG 840
 DB 781 GCGCTGAGCG 840
 QY 841 AAGAACTGCG 900
 DB 841 AAGAACTGCG 900
 QY 901 GACATCG 960
 DB 901 GACATCG 960
 QY 961 TTTGCGCTGCG 1020
 DB 961 TTTGCGCTGCG 1020
 QY 1021 GAGCTGCG 1080
 DB 1021 GAGCTGCG 1080
 QY 1081 AATGCGATGCG 1140
 DB 1081 AATGCGATGCG 1140
 QY 1141 ATGCGTGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 DB 1141 ATGCGTGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 QY 1201 ATCATCGCGCAAC 1212
 DB 1201 ATCATCGCGCAAC 1212

RESULT 6
 US-10-251-078-15
 Sequence 15, Application US/10251078
 Publication No. US20030119084A1
 GENERAL INFORMATION:
 APPLICANT: Roche Diagnostics GmbH
 APPLICANT: Shao, Zhixin
 APPLICANT: Schmuck, Rainer
 APPLICANT: Kratzsch, Peter
 APPLICANT: Kenkies, Janet
 APPLICANT: Weisner, Harald
 TITLE OF INVENTION: Variants of an Erwinia-type creatinase
 FILE REFERENCE: 20981 EP
 CURRENT APPLICATION NUMBER: US/10/251,078
 CURRENT FILING DATE: 2002-09-20
 NUMBER OF SEQ. ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 SEQ. ID NO. 15
 LENGTH: 1215
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: variant CT2m28
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1215)
 US-10-251-078-15

Query Match 80.6%; Score 976.8; DB 15; Length 1215;
 Best Local Similarity 87.9%; Pred. No. 1.7e-252;
 Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 ATGACTGACGACATGTTGACGTGATGAAATGSCAACACGCGGAGAAAGATTATTCGCGG 60
 DB 1 ATGACTGACGACATGTTGACGTGATGAAATGSCAACATGATGAGAAAGATTATTCGCGG 60

QY 61 TTTTCGATGCGGAGATGACCCGCGCAAAAGAGCTTCGCGGTGATGCGCAAGAC 120
DB 61 TTTTCGATGCGGAGATGACCCGCGCAAGAGCTTCGCGGTGATGCGCAAGAC 120
QY 121 AATGTCGATGCGGCGCTGTTCACTTTTATCATGTCATCACTATTTCCGCTGCTG 180
DB 121 GAGTCGATGCGGCGCTGTTCACTTTTATCATGTCATCACTATTTCCGCTGCTG 180
QY 181 TACTGCTATTTGCGAGCGCAAGTACGGCATGTCATGACCAACAACCCGCAAGCAT 240
DB 181 TACTGCTATTTGCGAGCGCAAGTACGGCATGTCATGACCAACAACCCGCAAGCAT 240
QY 241 TCGGCGCGGATGAGCGGCGCGAGCCCTGCGCGCGAGTTTGGGCGCAACAATCACTTAC 300
DB 241 TCGGCGCGGATGAGCGGCGCGAGCCCTGCGCGCGAGTTTGGGCGCAACAATCACTTAC 300
QY 301 ACCGACTGCGCGCGCAATTTCTATCGCGCGTGCAGCTGACCAACCGGCGCGCAAG 360
DB 301 ACCGACTGCGCGCGCAATTTCTATCGCGCGTGCAGCTGACCAACCGGCGCGCAAG 360
QY 361 CGCATGCGCATGAGTTTCAACAAGTTCGACTTCCGCGCGCACTGAGAGAGCC 420
DB 361 CGCATGCGCATGAGTTTCAACAAGTTCGACTTCCGCGCGCACTGAGAGAGCC 420
QY 421 CTACCGGCGGTGAGCTTCTGACATCAGCCGCTGATGATGAGTGGCAACATCAAG 480
DB 421 CTACCGGCGGTGAGCTTCTGACATCAGCCGCTGATGATGAGTGGCAACATCAAG 480
QY 481 TCGCTCGAAGAGCAGAGCTGATCGCGAGAGCGCGCGGTGATGACCTGCGCGCGCG 540
DB 481 TCGCTCGAAGAGCAGAGCTGATCGCGAGAGCGCGCGGTGATGACCTGCGCGCGCG 540
QY 541 GCGTCGCGGCGCTGATCAAGCGCGCGGTGCGCGAGCATGAGTGGCATGCGCACACC 600
DB 541 GCGTCGCGGCGCTGATCAAGCGCGCGGTGCGCGAGCATGAGTGGCATGCGCACACC 600
QY 601 AATGCGATGATCGCGGAGATGCGCAAAATGTTCCCTTGTGAGAGTGTATGACACTGAG 660
DB 601 AATGCGATGATCGCGGAGATGCGCAAAATGTTCCCTTGTGAGAGTGTATGACACTGAG 660
QY 661 ACCTGCTTCAGTTCGCGGATCAACCGAGCGCGCAATTCGCTTCAACAACCGCATC 720
DB 661 ACCTGCTTCAGTTCGCGGATCAACCGAGCGCGCAATTCGCTTCAACAACCGCATC 720
QY 721 GTGCAATTCGCGGATCACTTTTGTCTCAACACTTTCGCGATATCTTGGCTATCAACC 780
DB 721 GTGCAATTCGCGGATCACTTTTGTCTCAACACTTTCGCGATATCTTGGCTATCAACC 780
QY 781 GCGCTGAGGCGGACGCTGTTCTGCGACCATGTCGATGACGCGAGCTGACACTTGGAG 840
DB 781 GCGCTGAGGCGGACGCTGTTCTGCGACCATGTCGATGACGCGAGCTGACACTTGGAG 840
QY 841 AAGAAGTGGCGGCGGATGCGCGGCGCTGAGCTGATCAACCGGCGCGCGCTGCAAG 900
DB 841 AAGAAGTGGCGGCGGATGCGCGGCGCTGAGCTGATCAACCGGCGCGCGCTGCAAG 900
QY 901 GACATGCGCATGAGTCAAGATGACCGCGAGTGGGACCTGCTGAAGTACCGCTTC 960
DB 901 GATATGCGCCTCGAATCAAGATGACCGCGAGTGGGATCTGCTGAAGTACCGCTTC 960
QY 961 TTTGCGCTATGCGGCACTTCTTGGCGGCTGCTGCTCACTATGAGTTCGAGGCGCGG 1020
DB 961 TTTGCGCTATGCGGCACTTCTTGGCGGCTGCTGCTCACTATGAGTTCGAGGCGCGG 1020
QY 1021 GAGTCGCGGAGATGACCAACCGAGCTGAGAGCCGCGCATGCTGCTCAATGAGAGCCG 1080
DB 1021 GAGTCGCGGAGATGACCAACCGAGCTGAGAGCCGCGCATGCTGCTCAATGAGAGCCG 1080
QY 1081 AATGTCGATGCTCCGAGGCGCATGCGCGGTGCGCGGCTTATGCGAGAGCATCTCTG 1140
DB 1081 AATGTCGATGCTCCGAGGCGCATGCGCGGTGCGCGGCTTATGCGAGAGCATCTCTG 1140
QY 1141 ATGCTCGGAGAGAGGCTGCGAGAACATCACCGGCTTCCGCTGCGGAGTCAACACC 1200

DB 1141 ATGCTCGGAGAGAGGCTGCGAGAACATCACCGGATTCCTTCCGCGCTGAGAGCAAC 1200
QY 1201 ATCATCGGCAAC 1212
DB 1201 ATCATCGGCAAC 1212
RESULT 7
US-10-251-078-21
; Sequence 21, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
; APPLICANT: Schmuck, Rainer
; APPLICANT: Kratzsch, Peter
; APPLICANT: Kenkies, Janet
; APPLICANT: Weisner, Harald
; TITLE OF INVENTION: Variants of an Erwinia-type creatinase
; FILE REFERENCE: 20981 EP
; CURRENT FILING DATE: US/10/251,078
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variant C7ed7
; NAME/KEY: CDS
; LOCATION: (1)..(1212)
US-10-251-078-21
Query Match 80.5%; Score 975.2; DB 15; Length 1212;
Best Local Similarity 87.8%; Pred. No. 4.7e-252;
Matches 1064; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 1 ATGACTGACGACATGTTGACGATGATGAATGACCAACCGCGAGAAAGATTATTCGCG 60
DB 1 ATGACTGACGACATGTTGACGATGATGAATGACCAACCGCGAGAAAGATTATTCGCG 60
QY 61 TTTTCGATGCGGAGATGACCCGCGCAAAAGAGCTTCGCGGTGATGCGCAAGAC 120
DB 61 TTTTCGATGCGGAGATGACCCGCGCAAAAGAGCTTCGCGGTGATGCGCAAGAC 120
QY 121 AATGTCGATGCGGCGCTGTTCACTTTTATCATGTCATCACTATTTCCGCTGCTG 180
DB 121 AATGTCGATGCGGCGCTGTTCACTTTTATCATGTCATCACTATTTCCGCTGCTG 180
QY 181 TACTGCTATTTGCGAGCGCAAGTACGGCATGTCATGACCAACAACCCGCAAGCAT 240
DB 181 TACTGCTATTTGCGAGCGCAAGTACGGCATGTCATGACCAACAACCCGCAAGCAT 240
QY 241 TCGGCGCGGATGAGCGGCGCGAGCCCTGCGCGCGAGTTTGGGCGCAACAATCACTTAC 300
DB 241 TCGGCGCGGATGAGCGGCGCGAGCCCTGCGCGCGAGTTTGGGCGCAACAATCACTTAC 300
QY 301 ACCGACTGCGCGCGCAATTTCTATCGCGCGTGCAGCTGACCAACCGGCGCGCAAG 360
DB 301 ACCGACTGCGCGCGCAATTTCTATCGCGCGTGCAGCTGACCAACCGGCGCGCAAG 360
QY 361 CGCATGCGCATGAGTTTCAACAAGTTCGACTTCCGCGCGCACTGAGAGAGCC 420
DB 361 CGCATGCGCATGAGTTTCAACAAGTTCGACTTCCGCGCGCACTGAGAGAGCC 420
QY 421 CTACCGGCGGTGAGCTTCTGACATCAGCCGCTGATGATGAGTGGCAACATCAAG 480
DB 421 CTACCGGCGGTGAGCTTCTGACATCAGCCGCTGATGATGAGTGGCAACATCAAG 480
QY 481 TCGCTCGAAGAGCAGAGCTGATCGCGAGAGCGCGGTGATGACCTGCGCGCGCG 540

Db 481 TCGCTCGAAGACAGAAAGCTGATCCGAGAGGTCGCCGATCTCGACACTCGGCGTCC 540
Qy 541 GCCTCGCGGCGCTGCCATCAAGGCGGCGCTGCCGAGCATGAAGTGGCGATCCGACCAAC 600
Db 541 GCCTCGGTTGGCCGCGTCAAGGCGGCGCTGCCGAGCAAGAGTGGCGATCCGACCAAC 600
Qy 601 AATGGATGATCCGCGAGATCGCCCAATGTTCCCTTGTGTGAGTGTATGACACCTGG 660
Db 601 AATGGGATGATCCGCGAGATCGCCCAAGTGTTCCTTGTGTGAGTGTATGACACCTGG 660
Qy 661 ACCTGATTCAGTCCGCGGCTCAACACCGAGCGGCGCACAATCCGCTCAACACCGCATC 720
Db 661 ACCTGATTCAGTCCGCGGCTCAACACCGAGCGGCGCACAATCCGCTCAACACCGCATC 720
Qy 721 GTGCAATCGGCGGAGATCTTTCGCTCAACACTTCCGATGATCTTCCGCTACTACAAC 780
Db 721 GTGCAATCGGCGGAGATCTTTCGCTCAACACTTCCGATGATCTTCCGCTACTACAAC 780
Qy 781 GCGCTGAGAGCGACGCTGTTCTGCAACCATGTCGATGACGCAAGCTTCGACATCTGGAG 840
Db 781 GCGCTGAGAGCGACGCTGTTCTGCAACCATGTCGATGACGCAAGCTTCGACACTGGAG 840
Qy 841 AAGAACTGGCGGCTGATCGCGGCGCTCGAGCTGATCAAGCGGCGCGGCGCTGCAAG 900
Db 841 AAGAACTGGCGGCTGATCGCGGCGCTCGAGCTGATCAAGCGGCGCGGCGCTGCAAG 900
Qy 901 GACATCGGCATCGAGCTCAACGAGATGTACCGCGAGTGGAGCTCTGAAAGTACCGCTCC 960
Db 901 GATATCGGCATCGAGCTCAACGAGATGTACCGCGAGTGGAGCTCTGAAAGTACCGCTCC 960
Qy 961 TTCGCTATGCGCACTCTTCCGCGCTGCTGCTCACTACAGTGGCGGCGGCGCTG 1020
Db 961 TTCGCTATGCGCACTCTTCCGCGCTGCTGCTCACTACAGTGGCGGCGGCGCTG 1020
Qy 1021 GAGCTGGCGGAGGAGATCGACACCGAGCTGAAGCGCGGATGTTCTCCATGAGGCG 1080
Db 1021 GAGCTGGCGGAGGAGATCGATACCGTGTGCAAGCGCGGATGTTCTCCATGAGGCG 1080
Qy 1081 ATGTGATGCTGCTCGGAGGAGATGCGCGGCTGCGGCTGATCGGAGACGACATCTCTG 1140
Db 1081 ATGTGATGCTGCTCGGAGGAGATGCGCGGCTGCGGCTGATCGGAGAGACATCTCTG 1140
Qy 1141 ATGTGCGGAGAGAGCTGTCGAGAAATACCTGCTTCCGTTGCTCGGAGACACACC 1200
Db 1141 ATGTGCGGAGAGAGCTGTCGAGAGAAATACCTGCTTCCGTTGCTGAGACACACC 1200
Qy 1201 ATCATCGGCAAC 1212
Db 1201 ATCATCGGCAAC 1212

RESULT 8

US-10-251-078-19

Sequence 19, Application US/10251078

Publication No. US20030119084A1

GENERAL INFORMATION:

APPLICANT: Roche Diagnostics GmbH

APPLICANT: Shao, Zhixin

APPLICANT: Schneck, Rainer

APPLICANT: Kratzsch, Peter

APPLICANT: Kenkies, Janet

APPLICANT: Weisner, Harald

TITLE OF INVENTION: Variants of an Erwinia-type creatinase

FILE REFERENCE: 20981 EP

CURRENT APPLICATION NUMBER: US/10/251,078

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 1212

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:variant CTed2

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (1212)

us-10-251-078-19

Query Match 80.3%; Score 973.6; DB 15; Length 1212;

Best Local Similarity 87.7%; Pred. No. 1.3e-251;

Matches 1063; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 1 ATGACTGACGACATGTTGACGATGATGAAGGACCAACGCGGAGAGAAATATTCGCG 60
Db 1 ATGACTGACGACATGTTGACGATGATGAAGGACCAACATGATGATATTCCTCC 60
Qy 61 TTTTCGATGCGGAGATGACCGCGCGCAACGAGCTTCGCGCTGATGGCCAAAG 120
Db 61 TTTTCGATGCGGAGATGACCGCGCGCAACGAGCTTCGCGCTGATGGCCAAAG 120
Qy 121 AATGTCATGCGGCGCTGTTCACTCTTATCACTGATCAACTATATTCGGCTGCTG 180
Db 121 AATGTCATGCGGCGCTGTTCACTCTTATCACTGATCAACTATATTCGGCTGCTG 180
Qy 181 TACTGCTATTTGCGACGCAAGTACGAGATGAGTCAATGACCAACCAACGACGAT 240
Db 181 TACTGCTATTTGCGACGCAAGTACGAGATGAGTCAATGACCAACCAACGACGAT 240
Qy 241 TCGGCGGCGATCGACGCGGCGCAAGCTTCGCGCGGAGCTTCGCGCAACATCACTAC 300
Db 241 TCGGCGGCGATCGATGCGGCGCAAGCTTCGCGCGGAGCTTCGCGCAACATCACTAC 300
Qy 301 ACCGACTGCGCGCGGACATTTCTATGCGCGCTGCGCGAGCTGACCAAGCGGCGCAAG 360
Db 301 ACCGACTGCGCGCGGACATTTCTATGCGCGCTGCGCGAGCTGACCAAGCGGCGCAAG 360
Qy 361 CGCATCGGCGATCGAGTTGACCAAGTCAATCGACTTCGCGCGGAGCTTCGAGGAGCG 420
Db 361 CGCATCGGCGATCGAGTTGACCAAGTCAATCGACTTCGCGCGGAGCTTCGAGGAGCG 420
Qy 421 CTACCGGCGGCTGACCTTCTGTCGATGACCGAGCTTCGATGATGATGCGACATCAAG 480
Db 421 CTACCGGCGGCTGACCTTCTGTCGATGACCGAGCTTCGATGATGATGCGACATCAAG 480
Qy 481 TCGCTCGAAGAGCAAGCTGATCCGCGAGGCGCGCGCTGCTGATGATGATGCGCGCG 540
Db 481 TCGCTCGAAGAGCAAGCTGATCCGCGAGGCGCGCGCTGCTGATGATGATGCGCGCG 540
Qy 541 GCGTGGCGGCTGACATCAAGGCGGCGTGCAGGAGCAATGAAGTGGAGTGGCGACCAAC 600
Db 541 GCGTGGCGGCTGACATCAAGGCGGCGTGCAGGAGCAATGAAGTGGAGTGGCGACCAAC 600
Qy 601 AATGCGATGATCCGCGAGATGCGCAAAATGTTCCCTTCTGAGCTGATGAGACACTGG 660
Db 601 AATGCGATGATCCGCGAGATGCGCAAAATGTTCCCTTCTGAGCTGATGAGACACTGG 660
Qy 661 ACCTGTTTCCAGTGGGAGATCAACCGAGCGGCGCAATCCGCTGATCAACCGCATC 720
Db 661 ACCTGTTTCCAGTGGGAGATCAACCGAGCGGCGCAATCCGCTGATCAACCGCATC 720
Qy 721 GTGCAATCCGCGGAGATCTTTCGCTCAACACTTCCGATGATCTTGGGCTACTACAC 780
Db 721 GTGCAATCCGCGGAGATCTTTCGCTCAACACTTCCGATGATCTTGGGCTACTACAC 780
Qy 781 GCGCTGAGAGCGACGCTGTTCTGCGACCATGTCGATGACGCGAGCTTCGATCTGGAG 840
Db 781 GCGCTGAGAGCGACGCTGTTCTGCGACCATGTCGATGACGCGAGCTTCGATCTGGAG 840
Qy 841 AAGAACTGGCGCTGATCGCGCGGCTGAGCTGATCAAGCGGCGGCGCGCTGCAAG 900
Db 841 AAGAACTGGCGCTGATCGCGCGGCTGAGCTGATCAAGCGGCGGCGCGCTGCAAG 900
Qy 901 GACATCGCATCGAGCTCAACGAGATGATCGCGAGTGGAGCTGCTGAATGATCCGCTCC 960
Db 901 GACATCGCATCGAGCTCAACGAGATGATCGCGAGTGGAGCTGCTGAATGATCCGCTCC 960

Db 901 GATATCGCCATCGAACTCAAGAGATGTACCGGAGTGGATCTGTGAATGATCCGCTCC 960
Qy 961 TTGGCTATGGCCACTCTTGGCGTGTGTCACCTACTACGATCGGAGCGCGGCGTG 1020
Db 961 TTGGCTATGGCCACTCTTGGCGTGTGTCACCTACTACGATCGGAGCGCGGCGTG 1020
Qy 1021 GAAGCTCGGAGGACATCGATCGACCGAGCTGAAAGCCCGGCAATGATGATGAGCGG 1080
Db 1021 GAAGCTCGGAGGACATCGATCGACCGAGCTGAAAGCCCGGCAATGATGATGAGCGG 1080
Qy 1081 ATGTGTATGTGCGGAGGAGGATGCGCGGTGCGGCGGCGTATGCGGAGCAGCATCTTG 1140
Db 1081 ATGTGTATGTGCGGAGGAGGATGCGCGGTGCGGCGGCGTATGCGGAGCAGCATCTTG 1140
Qy 1141 ATGTGTGTGGAGAGAGCGGCGGAGGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 1141 ATGTGTGTGGAGAGAGCGGCGGAGGATGATGATGATGATGATGATGATGATGATGATG 1200
Qy 1201 ATCATCGGCAC 1212
Db 1201 ATCATCGGCAC 1212

RESULT 9
US-10-437-963-88003/c

/ Sequence 88003, Application US/10437963
/ Publication No. US20040123343A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ APPLICANT: Wu, Wei

/ APPLICANT: Boukharov, Andrey A.

/ APPLICANT: Barbazuk, Brad

/ APPLICANT: Li, Ping

/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

/ FILE REFERENCE: 38-21(53221)B

/ CURRENT APPLICATION NUMBER: US/10/437,963

/ CURRENT FILING DATE: 2003-05-14

/ NUMBER OF SEQ ID NOS: 204966

/ SEQ ID NO 88003

/ LENGTH: 2733

/ TYPE: DNA

/ ORGANISM: Oryza sativa

/ FEATURE:

/ OTHER INFORMATION: Clone ID: PAT_MRT4530_86897C.1

/ US-10-437-963-88003

Query Match 6.2%; Score 75.4; DB 17; Length 2733;
Best Local Similarity 44.4%; Pred. No. 3.8e-10;

Matches 399; Conservative 0; Mismatches 491; Indels 9; Gaps 2;

Qy 252 CGACGCGGCGCAAGCCCTGCGCGCGGAGCTTCCGCGCAACATCACTACCGACTGGCG 311
Db 2506 CGACGCGGCGGAGAGCGCGGAGGAGAGCGGCTTCCACTTCTACTGCGCCACTTCC 2447
Qy 312 CCGCAATTTCTTATCGCGCGGCGGCGGAGCTGACCAAGCGCGCGCAAGCGGATGGCAT 371
Db 2446 CGAGAGCGTGTCTTCTCCGTCAAGGTCCGCTGTCCGTCAAGCTCATCGGCGG 2387
Qy 372 CGAGTTGACGACGATCTGATCTGCGCGCGGAGGAGCGGAGCGGCGGCTTCCGCGGCT 431
Db 2386 CGCTTACTCTCCCGTCAAGGAGCTTCTGTCGCGGAGGCGGCTGAGCGGAGCTGACAT 2327
Qy 432 CGACTTGTGATCATGACGACGCGCTGATGTGATGCGGACCATCAAGTCCGCTGAGGA 491
Db 2326 CCGCGCGGCGGAGAGAGAGCTCCCGAGGTCGACATCAAGTCCGCTGAGGA 2267
Qy 492 GCGAGAGCTGATCGCGGAGGCGCGGCGGCTGTGTGAGCTGCGGCGGCGGCGCTGCGGCG 551
Db 2266 CAGGAGCGTGGCGCGCGGAGAGAGTGTGAGGCGGCGGCGGCTGCGGCGGCGGCGGCG 2207

Qy 552 TGCATCAAGGCGGCGGTGCCGAGCATGAATGGGATCGGACACCATGATGATGAT 611
Db 2206 GATCCCCGCGGTGCGGTGACCTTCTCAAGAGAGAGCGGAGTGAAGGATCACTGTA 2147
Qy 612 CCGGAGATGCGCAATGCTTCCCTGCGGAGGATGAGACACTGAGCTGTGTTCA 671
Db 2146 CAGGAGCGGCGGAGCGGAGAGCTTCCCGCGGAGAGATCCGCTGCGGCGGCGGAG 2087
Qy 672 GTGGGACATCAACCGAGCGGCGGAGATCCGCTGACCAACCGCATGTGCAATCCGG 731
Db 2086 CTACAGAGAGGCGGCGGTGAGAGAGCTGTTCACGCGCATCAACAGGAGGAGGAGG 2033
Qy 732 CGACATCTTGTGCTCAACACTTCCGATGATCTTCCGCTACTACCGCGCTGAGAGG 791
Db 2032 GACCTCATATATCATCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1973
Qy 792 CAGCTGTCTGCGACATGTCATGATGAGCGGAGCGGCTGACATCTGAGAGAGAGAG 851
Db 1972 GTCCCGGAGGCGGCGGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1913
Qy 852 CCGTATGCGGCGGCGGCTGAGCTGATCAAGCGGCGGCGGCGGCTGCAAGAGATGCGCAT 911
Db 1912 CGAGGCGTCCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1853
Qy 912 CGAGCTCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 971
Db 1852 CGCATCGGATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1793
Qy 972 CCATCTTCCGCGGTGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
Db 1792 CGAGGAGCTCGAGCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1733
Qy 1032 GAGCATGACACGAGCTGAGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
Db 1732 CAGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1673
Qy 1088 GCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1147
Db 1672 CGTGACACACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1614

RESULT 10

US-10-425-115-109294/c

/ Sequence 109294, Application US/10425115
/ Publication No. US20040214272A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants

/ FILE REFERENCE: 38-21(53222)B

/ CURRENT APPLICATION NUMBER: US/10/425,115

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 369326

/ SEQ ID NO 109294

/ LENGTH: 1262

/ TYPE: DNA

/ ORGANISM: Zea mays

/ FEATURE:

/ OTHER INFORMATION: Clone ID: MRT4577_31174C.1

/ US-10-425-115-109294

Query Match 6.1%; Score 73.4; DB 18; Length 1262;
Best Local Similarity 44.1%; Pred. No. 1.2e-09;

Matches 308; Conservative 0; Mismatches 391; Indels 0; Gaps 0;

Qy 205 GCGATGTGATGAC 264
Db 1107 GCGAGCGGCTCCGCTCCAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1048

QY 265 CCTGAGCGCCGAGCTTGGGCGACAACTACCTACCGGATGGCGCCGCAAAATTTC 324
DB 1047 AGCATGCGCTTCTACTCTGCGCCAGCAAGACTCTTCAAGCGCGCTGCGGCGATC 988
QY 325 TATCGCGCGCTGCGCGAGCTGACACACGGGCGCCAAAGCGCATCGGATCGAGTTTCAGCAC 384
DB 987 GGGCTGCGCTTGAAGTGGGCAACGGAAAGTGGCGAGCTGCGCGGACCCCGGCGAGC 928
QY 385 GTCAATCTGCACTTCCGCGCGAGCTCGAAGAGCCCTACCGGCGCTGCACTTCTGTCAGC 444
DB 927 GCGCGGCTCTGGGTCCGCGACAACGTCGAGGCTCTACCCGAGACGTGACATCAGGTAC 868
QY 445 ATGACCGAGCCCTCGATGTGATGTGGCACCATCAAGTGGCTGGAAGAGAGAACTGATC 504
DB 867 GTGCGTGTGGGAGCAAGAGTCTGCTCCCGCGCGCGCGCTGCTGCAAGGCAATGCAAGAC 808
QY 505 CGCGAAGGCGCCCGCGGTGTGACGTGCGCGCGCGCGCTGCGCGGCTGCTCAAGAGCC 564
DB 807 GTGACGCGCGCGCTGCGCTGCGCGCGCTGCGCGCGCGCTGCAAGGTGTCACGCGCGTC 748
QY 565 GCGGTGCGCGAGCATGAAGTGGCGATCGGCGACCAACATGCGATGTCGCGAGATCGCC 624
DB 747 AAGATGAGACGCGGTGACACACTCTCGCGCGCTGCGCGCGGTGTCAGGAGACCCCGCC 688
QY 625 AAATGCTTCCCTTGTGTGAGCTGATGACACTTGAACCTGTTCCAGTGGGCGATCAAC 684
DB 687 GCGATGTGCGCCATGCGCGAGTTCCTGCGCGCGCGCGCGCTGCTGCGCAACGTC 628
QY 685 ACCGAGCGCGCGCATCAATCGGTCACCAACCGCATGTGCAATCGGCGAGCATCTTTTCG 744
DB 627 TACCTTACTTTCGCGTCAAGTACAGGACGCGCGCATGACTTGAACCTGCTGTC 568
QY 745 CTCAACACCTTCCCGATGATCTTGGCTTACTACACGCGCGTGGAGCGCAGCTGTTTCG 804
DB 567 CAGCCAGCGCCAGCGAGTCAAGGACCCCGCAAGGCGGTGTGACGAACTCTTTC 508
QY 805 GACCATGTGATGAGCGCGCTGCACTGTGGAGAAAGTGGCGGTGATGCGCGC 864
DB 507 GACGCGATGTGAGCGCGCTGCGCGCGCGCTGCAAGGCGCGCGCGCGCGCGCTGTC 448
QY 865 GGGCTCGAGCTGATCAAGCGCGCGCGCGCTGCAAGGAC 903
DB 447 GACGTGTGTGTGTCGAGACCGGAGTGGCGCTGCGCGAC 409

RESULT 11

US-10-437-963-38426
Sequence 38426, Application US/10437963
Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 38426
LENGTH: 1483
TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_42062C.1
US-10-437-963-38426

Query Match

5.8%; Score 69.8; DB 17; Length 1483;

Best Local Similarity 44.9%; Pred. No. 1,1e-08;
Matches 266; Conservative 0; Mismatches 327; Indels 0; Gaps 0;

QY 587 CGATCGCACCAACCAATGCGATGATTCGCGAGATCGCCAAATGTTCCCTTGTGAGC 646
DB 309 CGAGACCGCGACGAGCGGAGATTCGCGCGCTTCACTCGCGGAGTACGACCTTC 368
QY 647 TGATGACACTGGAAGCTGTTCCAGTGGGATCAACACGAGCGCGCGCAATCCGG 706
DB 369 TCCGAGACTACCCCGAGGCTACTTCAACGAGCGCGCTTGGAGAGAGGCGAGG 428
QY 707 TCACCAACCGATGCGTGAATTCGCGGACATCTTTCGCTCAACACTTCCGATGATCT 766
DB 429 ATGACACGAGCATGCGCGGCAACGATGCTCCGCTTGAACCGCTTGGAGTACT 488
QY 767 TCGGCTACTACCGCGCTGAGCGCAAGCTTCTGCGACATGTGATGACGCGAGCC 826
DB 489 GCGCGGCTACCGCGCGGCTGTTGCTGCGCGCGCGCGCTTGTGACGCGCGCTCCG 548
QY 827 TCGACATTTGGAGAGAAAGTGGCGCTGCTGCTGCGCGCGCTGAGCTGATCAAGCCG 886
DB 549 ACATGCGCATCACTGCTCGCGCGGCGATGACACGCGCTGCGCAAGCGCACCGCT 608
QY 887 GCGCGCGCTGCAAGGACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGAGCTTC 946
DB 609 TCTGCTACGTCAAGACATCGTGTGCTGCGCATCAAGAGCTCTCGGCACTTCAGCGAG 668
QY 947 TGAAGTACCGCTCTTGTGCGTATGAGCGCATCTTTCGCGGTGCTGCTGCACTAGCGTC 1006
DB 669 TCATCTACGTGACATGACCGCGACACCGCGAGCGGCTGACAGACCTTCTTGAAGT 728
QY 1007 GCGAGCGCGGCTGAGCTGCGCGAGGACATGACACCGAGCTGAAGCGCGGAGTGG 1066
DB 729 CCAACCGGATGATGACGCTGCTGCTGCAACCGGTACGGAATACGCGCCCAAGAGCT 788
QY 1067 TCTCAGTACCGCATGAGTGTGCTGCGGAGGAGCATCCGCGTCCGCGGCTATCGCG 1126
DB 789 TCTTCCGCGCTTCGCGCGCATCAAGAAATCGGAGCGCGCGCGGAGCATACAGCG 848
QY 1127 AGCAGCATCTGATGCTGCGGAGAGAGCGGTGCGGAGACATCACCGGCTTC 1179
DB 849 TGAAGTCCCTTGGAGCGCGCGCTGCGGAGAGCTTACACAGCTGCTTC 901

RESULT 12

US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1

LENGTH: 9025608

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown

QY	842	AGAAAGTGGCGGTGATATGCGCGGGGCTCGAGCTGATCAAGCCGGGCGCGCTGCAAG	901
Db	18966	TCGAATCTGGATCCCGAAGCGGCTGCTGTCCCGCATATGCGCCAGAAATCTTCCGCGAAGGCG	190255
QY	902	ACATCGCCATCGAGCTCAACGAGATATGACCGGAGTGGAGGAGCTGTGAAGTACCGCTCT	961
Db	19026	CCGGCCCGCTGTCGCGCTGTGGCGAAGAACCGCCCCGAGAGCTCTCCGCCGTACCTGGCC	190855
QY	962	TCGGCTATGCGACACTCTTTCGGCGCTGCTGTGCACTATACGGTTCGAGCGCGCGCTGG	1021
Db	19086	TGGCCCGCGGCCACATGTCGGGGGCGTCAACGGTCCGCTGGGCGGGCCCTTTGAAAGGACCG	19145
QY	1022	AGCTGCCGGAAGACATGACACGAGCTGAAGCCCGGCATGTGTCTCCATGAGCCGA	1081
Db	19146	GCGGCGCGCGCGCGACCTGGCCACTACCCCTTTCAGCACGACGAGTCTTGGCGGACCG	19205
QY	1082	TGTGTATGTCTGCCGAAGGGCATATGCCCGGTATGCCGAGACGACATCTTGA	1141
Db	19206	CGGCCCGCGCGCCACCAAGACGTCAACCCCGCGGAGCTGGCGCGCCGACCAACCCGCTGC	19265
QY	1142	TCGTTCGGGGAAGACGATGCGCGAAGAACATCACCGGCTTCCCGTTTC	1185
Db	19266	TCGGCGCGCACCTGTGAATCTGCGCGACGCGGGCGAGCTATCTTTGTTTC	19309

RESULT 14
US-10-203

```

Sequence 35 Application US/10203295
Publication No. US20040115762A1
GENERAL INFORMATION:
APPLICANT: Zotchev, Sergey Borisovich
APPLICANT: Sekurova, Olga Nikolayivna
APPLICANT: Fjærevik, Espen
APPLICANT: Brautaset, Trygve
APPLICANT: Strom, Arne Reidar
APPLICANT: Valla, Svein
APPLICANT: Ellingsen, Trond Erling
APPLICANT: Sletta, Havard
APPLICANT: Gulliksen, Ole-Martin
TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their
FILE REFERENCE: 1181-265
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/GB 01/00509
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: GB 0009387.2
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 125401
TYPE: DNA
ORGANISM: Streptomyces nouraei ATCC 11455
US-10-203-295-35

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	Query Match	Similarity	5.7%;	Score 68.8;	DB 17;	Length 125401;
	Best Local	Similarity	42.8%;	Pred. No. 4.5e-08;		
	Matches	404;	Conservative	0;	Mismatches	517;
					Indels	3;
					Gaps	1;
Qy	245	CCGCGATTCGACGCGCGCCAGCCTTCGCGCGCAGCAATCACTTACACCG	304			
Db	78627	CCGCGCTTCGTCGCGTTCGAGTCCGCTTACCGCCTTCGTCGCGTCCCTCGCGTACCC	78686			
Qy	305	ACTGCGCGCGGACAAATTTCTATCGCGCGCGGCGCAGCTGACCAAGCGCCACAGCGA	364			
Db	78687	CCGACTTCGTCGCGCGCGCATCTTCATTCGCGAGCTTCGCGCGCGCGGACGTCGCGCGGTC	78746			
Qy	365	TCGGCATTCGATTCGACCAAGTCATCTCGATTCGCGCGCAGCTCGAGAGACCTTAC	424			

Db	78747	TTCTCCCTCGAAGACGCTGCAACCTCGTGGCCGCGCCGCGCTCATGCAAGGCTTC	78806
Qy	425	CGGCGCTGCACTTCGTGACATGACCGACGCCCTGATGTGGATGCGCACATCAAGTCG	484
Db	78807	CGCGGGGGGGCGGATGCTCGGATCCGGCCGACCGAGGACGAGGTCACCCCCACTCA	78866
Qy	445	TCGAAGACGAGAGCTATCCGGAAAGGCGCCGCGCTGTGTGACGTTCGGCGGCGGCTT	544
Db	78867	CCGACGACGTCTCATGCGCGCGGTCAACGGGCGCACTTCGCTGCTGTGGCGGCA	78926
Qy	545	GCGGGCGTCGCATGAAGCGCGGGGTGCCGAGCATGAAGGGGATGCGCACCAATG	604
Db	78927	AGGAAGCGTGGCTCGCATGGGCGGGLTTACCGCCGACGACCGCAAGACCAACCGGC	78986
Qy	605	CGATGATTCGGGAGATGCGCAAAATCGTTCCTTCGTGGAGCTGATGACACCTGGACCT	664
Db	78987	TGCGGGTACGACACGCTTCATCTCGCGGTCAATGACCGGATGCTGGGGAATTCGGG	79046
Qy	665	GGTTCAGTCGGGATCAACACGACGGCGGCGCAATCGG--TCACCAACCGCATG	721
Db	79047	CCGTGCGCGGGGCTGACTTACAGAGCGGCGCATCCGGTCTCTCAACTCACCG	79106
Qy	722	TGCAATCCGGCGACATCTTTCGCTCAACACTTCCGATGATCTTCGGCTACTACCG	781
Db	79107	GCACTGTCGCGCGCGCTGCGGACTGTGCTCCGCGACTGAGGTCGCCACATTCGCGG	79166
Qy	782	CGCTGAGACGACGCGTGTTCGACCATATGATGATACCGCACGCTCGACATCTGGAGAA	841
Db	79167	AGGGGCTCCGCTTCGCGGACGGGCTCACCGCTCACCGACCGCGGCTGACACAGCTG	79226
Qy	842	AGAACTGGGCTGTCATCGCGCGGGCTGAGCTGATCAAGCCCGGGCGCGCTGCAAG	901
Db	79227	TCGAATCGGACCGGACGGGCTGTCTCGGCAATGCGCAGGAATCTTCGCGGACGGG	79286
Qy	902	ACATCGGCATCGAGCTCAACGAAATGTAACCGGAGTGGGACCTGCGAAGTACCGCTCT	961
Db	79287	CCGCGCGCGTGGCGGCTGTGCGGCAAGACCGCCCGAGGAGCTTTCGCGCTCACGGGC	79346
Qy	962	TCGGCTATGACCACTCTTCGCGGCTGTGCGCATCACTACGAGTGGCGGACGCGGCTGG	1021
Db	79347	TGGCGCGCGCCACATGTCGCGGGGTCAAGGTTCGCTCGGGCCGGCTCTTTCACAGGACCG	79406
Qy	1022	AGCTGCGCGAAGCATTCGACCGAGCTGAAGCCCGGACGTGTGCTTCATGAGCCGA	1081
Db	79407	GCGGCGCGCGCGCGACATGCGCACCTTACGACCAACGAGGATCTGGCGGACCG	79466
Qy	1082	TGATGATGCTGCGGAGGGGATCCCGGTGCGGCGGCTATGCGGACCGACATCTGGA	1141
Db	79467	CGGCGCGCGCGCGCCGACGATCAACCGCGCGGAACTGGGCGCGCGCGACACCGCTGC	79526
Qy	1142	TCGTGCGGAGGAGCGGTGCGGAAATCAATCACGGGCTTCCGTTTC	1195
Db	79527	TCGGCGCCACGTCGTGAATCTGCGCAAGGAGCGGCTACTTGTTC	79570

RESULT 15

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US-10-437-963-57011/c
: Sequence 57011, Application US/10437963
: Publication No. US20040123343A1
:
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Barbazuk, Brad
: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221) B
: CURRENT APPLICATION NUMBER: US/10/437,963

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; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 57011
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58865C.1
US-10-437-963-57011

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Query Match      5.7%; Score 68.6; DB 17; Length 1169;
Best Local Similarity 45.3%; Pred. No. 2.2e-08;
Matches 248; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

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DB 918 GCGGCGGCGCGCCAGCGCGCGCGCGCAACAGCGCGTCTCCCGCTACTGGGACAGCGCC 859
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 GCCACCAACCAATGCGATGATCGCGAGATCGGCAATGTTCCCGTGTGGAGCTGATG 651
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DB 858 AACCTGTCCCGCGCCAGCTCGCGCGCTCAAGCGCGCGCACCTCACTCAGCGTCATG 799
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QY 652 GACACCTGAGCTGTTCAGTCCGCGCATCAACCGAGCGCGCGCACATCCGGTCAAC 711
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DB 798 GTGCGGCTCGGCGGAGACGCGTGAAGACACCGCAAGTCTTCTTCCCGAAGCTCC 739
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QY 712 AACCGATGTGCAATCCGCGCATCTTTGCTCAACACTTCCCGATGATCTTCCGC 771
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DB 738 GTGACTCGTGGTGGCCCAACGCGCTCGCTCCGTCCTCGGATCATCGACGCTTACGCGC 679
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QY 772 TACTACACCGCGCTGAGGCAAGCTGTTCTGAGACCATGTGATGACGCGAGCTCGAC 831
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DB 678 CTCGACGCGCTGACGCTGACCTACGAGCACTTCAACGACGACGCGCGCGCGCTGAC 619
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QY 832 ATCTGGAGAGAAAGTGGCGCTGCAATCGCCGCGGCTGAGCTGATCAAGCCGGGCGCG 891
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DB 618 AGTTGATGAGTGAATCGCGCGCTCTCACCGAGCTCAAGCGCGGCAACCGAATC 559
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QY 952 TACCGCTCTCTGGGCTATGAGCACTCTTGGGCGTGTGCACTACTAGAGGTGCGGAG 1011
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DB 498 CGGCGCTACGCGCGGTGATGACCTCTGTAACCTTCAAGCTTACGCGTACGCGCAACAC 439
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DB 438 ACCGAGTGGCGGACGTAAGTGTCTTACGAGGAGGAGCGGCGGAATACCGGGGCGGC 379
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QY 1072 ATGAGC 1078
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DB 378 AAGTGC 372
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Search completed: November 19, 2004, 16:26:43
Job time : 692 secs

	Query Match	99.9%;	Score 1210.4;	DB 6;	Length 1212;
	Best Local Similarity	99.9%;	Pred. No. 2.6e-145;		
	Matches 1211;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATGACTGACGACATGTTTGCAAGTATGAAATGGCACAACGGCGAGAAAGATTATTTCGGCG	60		
Db	1	ATGACTGACGACATGTTTGCAAGTATGAAATGGCACAACGGCGAGAAAGATTATTTCGGCG	60		
Qy	61	TTTTTCGATGCCGAGATGATGACCCCGCCGCAAAACGACGTTGGCGGCTGATGGCCCAAGAC	120		
Db	61	TTTTTCGATGCCGAGATGATGACCCCGCCGCAAAACGACGTTGGCGGCTGATGGCCCAAGAC	120		
Qy	121	AATGTGATCGAGGGGCGCTGTTCACCTCTTATCACTGATCACTACTATTCGGCGTGCGTG	180		
Db	121	AATGTGATCGAGGGGCGCTGTTCACCTCTTATCACTGATCACTACTATTCGGCGTGCGTG	180		
Qy	181	TACTGCTATTTTCGACGCAAGTAACGGCATGATCAATGACCAACAACGCCACGACGATT	240		
Db	181	TACTGCTATTTTCGACGCAAGTAACGGCATGATCAATGACCAACAACGCCACGACGATT	240		
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Db      241 TCGCGCGCATCGACGGCGGCGCAGCCCTGGCGCGCAGCTTGGCGCAACATCAGCTAC 300
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Db      301 ACCGATCGCGCGCGCGCAATTTCTATCGGCGCGCTGGCGCACTGACACAGCGCGCAAG 360
QY      361 CGCATCGGCGCATCGAGTTTCAGACGATCTGCACTTCGCGCGCGCAGCTCGAGAGCC 420
Db      361 CGCATCGGCGCATCGAGTTTCAGACGATCTGCACTTCGCGCGCGCAGCTCGAGAGCC 420
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Db      421 CTACCGGCGCTGCACTTCGTCATCAGCAGCAGCTTCGATGTGATGTGCAATCAAG 480
QY      481 TCGCTGGAAGAGAGAGAGCTGATTCGCGGAGAGGCGCGCGTGTGTGATCGTGGCGCGG 540
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Db      601 AATGCGATGATCGCGGAGATTCGCAAAATGCTTCCTTCGTGAGCTGATGGAACACTGG 660
QY      661 ACCTGTTGCACTCGGCGCATCAACACGAGCGCGCGCAAAATTCGGTTCACCAACCGCATC 720
Db      661 ACCTGTTGCACTCGGCGCATCAACACGAGCGCGCGCAAAATTCGGTTCACCAACCGCATC 720
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QY      781 GCGCTGAGAGCGACCGCTGTTCTGCGACCATGTGATGAGCGCAGCTTCGATGAGAG 840
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QY      841 AAGAACGTGCGCGTGCATCGCGCGCGGCTCGAGCTGATCAACCGCGCGCGCGCTGCAAG 900
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QY      901 GACATCGCGCATCGAGCTCAACGAGATGTACCGCGAGTGGACCTGTGTAAGTACCGCTCC 960
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Db      1021 GAGCTGCGCGAGGAGATCGACACGAGCTGAGAGCGCGGATGTGTCTCCATGAGAGCG 1080
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Db      1081 ATGTGATGCTGCGCGAGGCGCATGCGCGGCTGCGCGCTATCGAGAGCAGCATCTCTG 1140
QY      1141 ATGCTGCGGAGAGAGCGTGTGCGAGAACATCACCGGCTTCCTGCTCGGAGACACAC 1200
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QY      1201 ATCATCGGCAAC 1212
Db      1201 ATCATCGGCAAC 1212

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RESULT 2
E12280      1212 bp      DNA      linear      PAT 27-APR-1998
LOCUS      E12280
DEFINITION DNA encoding Alcaligenes thermostable creatin amidinohydrolase.
ACCESSION E12280
VERSION E12280.1 GI:3251114

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KEYWORDS JP 1996308579-A/1.
SOURCE Alcaligenes faecalis
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Alcaligenes.
REFERENCE 1 (bases 1 to 1212)
AUTHORS Sogabe, A., Yamamoto, K. and Kawamura, Y.
TITLE GENE ENCODING CREATINE AMIDINOHYDROLASE
JOURNAL Patent: JP 1996308579-A 1 26-NOV-1996;
TOYOBO CO LTD
COMMENT OS Alcaligenes faecalis
PN JP 1996308579-A/1
PD 26-NOV-1996
PF 16-MAY-1995 JP 1995117283
PT SOGABE ATSUSHI, YAMAMOTO KAZUMI, KAWAMURA YOSHINISU PC
C12N15/09, C12N1/21, C12N9/78, (C12N15/09, C12R1:05), (C12N1/21, PC
C12R1:425),
PC (C12N9/78, C12R1:425);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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/db_xref='taxon:511'
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Query Match 99.9%; Score 1210.4; DB 6; Length 1212;
Best Local Similarity 99.9%; Pred. No. 2.6e-145;
Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACTGACGACATGTTGCAAGTATGATGAAATGAGCAACGCGCGAGAAAGATTATTCGCG 60
Db 1 ATGACTGACGACATGTTGCAAGTATGATGAAATGAGCAACGCGCGAGAAAGATTATTCGCG 60
QY 61 TTTTCGATGCGAGATGACCGCGCGCAAAACGATTCGCGCTGAGTGGCCAAAGAC 120
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QY 121 AATGTGATGAGGCGCTGTTCACTCTTATACATGCACTACTACTATTCGCGCTGCTG 180
Db 121 AATGTGATGAGGCGCTGTTCACTCTTATACATGCACTACTACTATTCGCGCTGCTG 180
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Db 241 TCGGCGGCGATCGACGCGCGCAGCCTGCGCGCGCAGCTTCGCGCAACATCACTAC 300
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Db 361 CGCATCGGCGCATCGAGTTTCAGACGATCTGCACTTCGCGCGCGCAGCTCGAGAGCC 420
QY 421 CTACCGGCGCTGCACTTCGTCATCAGCAGCAGCTTCGATGTGATGTGCAATCAAG 480
Db 421 CTACCGGCGCTGCACTTCGTCATCAGCAGCAGCTTCGATGTGATGTGCAATCAAG 480

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 DB 541 GCCTGCGGCGCTGCCATCAAGCGCGCGCGCGAGCATGAAGTGGCATGCCACAC 600
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 DB 721 GTGCAATCCGGCGCATCTTTTCGCTCAACACCTTCCCGAGATGTTGGCTACTACAC 780
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 DB 781 GCGCTGAGCGGACGCTGTTCTGCGACCATGTGATGACGCCAGCTCGACATCTGGAG 840
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 QY 901 GACATCCGCATCGAGCTCAAGAGATGTACCGCGAGTGGAGACTTGTAAATACCGCTCC 960
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RESULT 3

E13584 1212 bp DNA linear PAT 27-APR-1998
 LOCUS E13584
 DEFINITION Alcaligenes faecalis gene for creatine amidinohydrolase.
 ACCESSION E13584
 VERSION E13584.1 GI:3252389
 KEYWORDS JP 1997215494-A/1
 SOURCE JP 1997215494-A/1
 ORGANISM Alcaligenes faecalis
 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Alcaligenes.

REFERENCE

1. (bases 1 to 1212)
 Sogabe, A., Hattori, T., Nishiy, Y. and Kawamura, Y.
 NEW CREATINE AMIDINOHYDROLASE, ITS PRODUCTION AND ITS USE
 Patent: JP 1997215494-A 1 19-AUG-1997;
 TOYOBO CO LTD
 OS Alcaligenes faecalis
 PN JP 1997215494-A/1
 PD 19-AUG-1997
 PF 13-FEB-1996 JP 1996025435

PI SOGABE ATSUSHI, HATTORI TAKASHI, NISHIYA YOSHIAKI, PI
 KANAMURA YOSHIOHISA
 PC C12N9/78, C12N15/09, (C12N9/78, C12R1:05), (C12N15/09, C12R1:19);
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 CC topology: Linear;
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ORIGIN
 Query Match 99.9%; Score 1210.4; DB 6; Length 1212;
 Best Local Similarity 99.9%; Pred. No. 2,66-145;
 Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACTGACGACATGTTGACAGTGATGAATGACAAACGCGGAGAAAGATTATTCGCG 60
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 QY 61 TTTTCGATGCGGAGATGACCCCGCGCAAAAGACGTTCCGGCTGATGGCCCAAGAC 120
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 DB 661 ACCGTGTTCCAGTGGGAGCATCAACGAGCGCGCGCAATCCGGTACCAACCGCATC 720
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DB 1201 ATCATCGGCAAC 1212

RESULT 4
LOCUS E16405 1212 bp DNA linear PAT 28-JUL-1999
DEFINITION Alcaligenes faecalis gene for creatine amidinohydrolase.
ACCESSION E16405
VERSION E16405.1 GI:5711088
KEYWORDS JP 1998174585-A/1.
SOURCE Alcaligenes faecalis
ORGANISM Alcaligenes faecalis
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Alcaligenes.
REFERENCE 1 (bases 1 to 1212)
AUTHORS Sogabe,A., Nishiyu,Y. and Kawamura,Y.
TITLE STABLE CREATINE AMIDINOHYDROLASE
JOURNAL Parent: JP 1998174585-A 1 30-JUN-1998;
TOYOBO CO LTD
OS Alcaligenes faecalis
PN JP 1998174585-A/1
PD 30-JUN-1998
PI 17-DEC-1996 JP 1996337027
PI SOGABE ATSUSHI, NISHIYA YOSHIKI, KAWAMURA YOSHIOHISA PC
C12N9/78 C07H21/04, C12N1/21, C12N15/09//C1201/34, C12N9/78, PC
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PC (C12N1/21, C12R1.19);
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CC topology: Linear;
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DB 601 AATGCGATGATCGCGGAGATCGCGAATCGTTCCTTCTGAGAGCTGATGATGATGATGATGATGAT 660
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RESULT 5
BD017699

LOCUS BD017699 1212 bp DNA linear PAT 27-AUG-2002
DEFINITION Gene encoding creatine amidinohydrolyase.
ACCESSION BD017699
VERSION BD017699.1 GI:22558875
KEYWORDS JP 2001252088-A/1.
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 1212)
AUTHORS Sogabe,A., Yamamoto,K. and Kawamura,Y.
TITLE Gene encoding creatine amidinohydrolyase
JOURNAL Patent: JP 2001252088-A 1 18-SEP-2001;
TOYOBO CO LTD
COMMENT OS Alkaligenes faecalis TE3581 (FERM P14237)
PN JP 2001252088-A/1
PD 18-SEP-2001
PF 26-FEB-2001 JP 2001051054
PI ATSUSHI SOGABE,KAZUMI YAMAMOTO,YOSHIHISA KAWAMURA PC
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ORIGIN
Query Match 99.9%; Score 1210.4; DB 6; Length 1212;
Best Local Similarity 99.9%; Pred. No. 2.6e-145;
Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
BD105662

LOCUS BD105662 1212 bp DNA linear PAT 27-AUG-2002
DEFINITION Stable creatine amidinohydrolyase.
ACCESSION BD105662
VERSION BD105662.1 GI:22651236

KEYWORDS JP 2001346594-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1212)
AUTHORS Sogabe, A., Nishiyama, Y. and Kawamura, Y.
TITLE Stable creatine amidinohydrolyase
JOURNAL Patent: JP 2001346594-A 1 18-DEC-2001;
TOYOBO CO LTD
OS Alcaligenes faecalis
PN JP 2001346594-A/1
PD 18-DEC-2001
PF 19-APR-2001 JP 2001121708
PI ATSUSHI SOGABE, YOSHIKAZU NISHIYAMA, YOSHIOHISA KAWAMURA, PC
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Best Local Similarity 99.9%; Pred. No. 2.6e-145;
Matches 1211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 ATGACTGACGACATGTTGACGATGAAATGACACACGCGGAGAAAGATTATTCGCG 60
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DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
Koyama, Y. and Furukawa, K.
Submitted (05-AUG-1998) Yasuji Koyama, Kikoman Corporation,
Research and Development, Noda 399, Noda, Chiba 278-0037, Japan
(E-mail: daisi-k@noda2.so-net.ne.jp, Tel: +81-471-23-5571,
Fax: +81-471-23-5959)
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ORIGIN

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Query Match      99.5%; Score 1205.6; DB 1; Length 1215;
Best Local Similarity 99.7%; Pred. No. 1,1e-144;
Matches 1208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 8
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LOCUS      E1155              1215 bp    DNA              linear      PAT 29-SEP-1997
DEFINITION gDNA encoding creatine amidinohydrolase.
ACCESSION  E1155.1 GI:22024796
VERSION    E1155.1 GI:22024796
KEYWORDS   JP 1996089255-A/1.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 1215)
AUTHORS   Furukawa,K., Ichikawa,T., Suzuki,M. and Koyama,T.
TITLE     NOVEL, CREATINE AMIDINOHYDROLASE GENE, NOVEL, RECOMBINANT DNA AND
          PRODUCTION OF CREATINE AMIDINOHYDROLASE
JOURNAL    Patent: JP 1996089255-A 1 09-Apr-1996;
          KIKKOMAN CORP
COMMENT    OS Alcaligenes sp. KS-85
          PN JP 1996089255-A/1
          PD 09-APR-1996
          PF 29-SEP-1994 JP 1994235737
          PI FURUKAWA KEISUKE, ICHIKAWA TOSHIO, SUZUKI MASARU, KOYAMA TAIJI
          PC C12N15/09,C12N9/78,(C12N9/78,C12R1:05),(C12N9/78,C12R1:19); CC
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ORIGIN

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Query Match      97.8%; Score 1184.8; DB 6; Length 1215;
Best Local Similarity 98.6%; Pred. No. 4.8e-142;

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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
Enterobacteriaceae; Erwinia.			
REFERENCE			
1 Shao, Z., Schmuck, R., Kratzsch, P., Kenkies, J. and Weisner, H.			
AUTHORS			
TITLE			
JOURNAL			
Roche Diagnostic GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)			
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Best Local Similarity 81.0%; Score 981.6; DB 6; Length 1215;			
Matches 1068; Conservative 0; Mismatches 144; Indels 0; Gaps 0;			
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RESULT 10
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LOCUS AX721949 1215 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 17 from Patent EP1298213.
ACCESSION AX721949
VERSION AX721949.1 GI:30422525

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KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 Shao,Z., Schneck,R., Kratzsch,P., Kenkies,J. and Weisser,H.
AUTHORS Variants of an erwinia-type creatinase
TITLE Patent: EP 1298213-A, 17 07-APR-2003.
JOURNAL Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
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ORIGIN

Query Match 81.0%; Score 981.6; DB 6; Length 1215;

Best Local Similarity 88.1%; Pred. No. 3.9e-116;

Matches 1068; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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RESULT 11

AX721941

LOCUS AX721941 1215 bp DNA linear PAT 07-MAY-2003

DEFINITION Sequence 9 from Patent EP1298213.

ACCESSION AX721941

VERSION AX721941.1 GI:30422517

KEYWORDS

SOURCE

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Shao,Z., Schmock,R., Kratzsch,P., Kenkiles,J. and Weisner,H.

TITLE Variants of an erwinia-type creatinase

JOURNAL Patent: EP 1298213-A 9 02-APR-2003;

Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)

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LOCUS AX721943
DEFINITION Sequence 11 from Patent EP1298213.
ACCESSION AX721943
VERSION AX721943.1 GI:30422519
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Shao, Z., Schmuck, R., Kratzsch, P., Kenkies, J. and Weisser, H.
TITLE Variants of an erwinia-type CreA/linase
JOURNAL Patent: EP 1298213-A 11 02-APR-2003;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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ACCESSION AX721945
VERSION AX721945.1 GI:30422521
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SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Shao Z., Schmuck R., Kratzsch P., Kenklies J. and Weisner H.
AUTHORS
TITLE
JOURNAL
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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ORIGIN
Query Match 80.6%; Score 976.8; DB 6; Length 1212;
Best Local Similarity 87.9%; Pred. No. 1.6e-115;
Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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RESULT 14
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LOCUS Sequence 15 from Patent EP1298213.
ACCESSION AX721947
VERSION AX721947.1 GI:30422523
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Shao Z., Schmuck R., Kratzsch P., Kenklies J. and Weisner H.
AUTHORS
TITLE
Variants of an erwinia-type creatinase

JOURNAL Patent: BP 1298213-A 15 02-APR-2003;
Roche Diagnostics GmbH (DE) ; F.HOFMANN-LA ROCHE AG (CH)

FEATURES

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Location/Qualifiers

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ORIGIN

Query Match 80.6%; Score 976.8; DB 6; Length 1215;
Best Local Similarity 87.9%; Pred. No. 1.6e-115;
Matches 1065; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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DEFINITION Sequence 21 from Patent EP1298213.
ACCESSION AX721953
VERSION AX721953.1 GI:30422529
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1 Shao,Z., Schmuck,R., Kratzsch,P., Kenklies,J. and Weisser,H.
AUTHORS
TITLE Variants of an erwinia-type crealtnase
JOURNAL Patent: BP 1298213-A 21 02-APR-2003;
Roche Diagnostics GmbH (DE) ; F.HOFMANN-LA ROCHE AG (CH)

FEATURES

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Query Match 80.5%; Score 975.2; DB 6; Length 1212;
Best Local Similarity 87.8%; Pred. No. 2,6e-115;
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